

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 03:55:57 ; Search time 267 Seconds
(without alignments)
9574.787 Million cell updates/sec

Title: US-10-088-092A-29
Perfect score: 487
Sequence: 1 ctgcttctctgtctgctt.....ggccaccacccgcctgtcga 487

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Genesegq23sep04:*
- 2: Genesegq1980s:*
- 3: Genesegq1990s:*
- 4: Genesegq2000s:*
- 5: Genesegq2001as:*
- 6: Genesegq2001bs:*
- 7: Genesegq2002as:*
- 8: Genesegq2002bs:*
- 9: Genesegq2003as:*
- 10: Genesegq2003bs:*
- 11: Genesegq2003cs:*
- 12: Genesegq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	100.0	487	5 AAF77401	Aaf77401 Human pho
2	308.6	63.4	883	3 AAF773130	Aaa73130 Mouse sec
3	308.6	63.4	883	5 AAF77387	Aaf77387 Murine cD
4	190.4	39.1	320	3 AAF773117	Aaa73117 Mouse sec
5	190.4	39.1	320	5 AAF77374	Aaf77374 Murine cD
6	144	29.6	180550	10 ADL13850	Adl13850 Osteoarth
7	108.8	22.3	1160	5 ABV22259	Abv22259 Human pro
8	108.8	22.3	1160	5 ABV28036	Abv28036 Human pro
9	108.8	22.3	1160	5 ABV23366	Abv23366 Human pro
10	108.8	22.3	1160	5 ABV29244	Abv29244 Human pro
11	108.8	22.3	1160	5 ABV23388	Abv23388 Human pro
12	108.8	22.3	1160	5 ABV25535	Abv25535 Human pro
13	108.8	22.3	1160	5 ABV29221	Abv29221 Human pro
14	107.2	22.0	435	10 ADL13848	Adl13848 Osteoarth
15	107.2	22.0	435	10 ADL13847	Adl13847 Osteoarth
16	107.2	22.0	779	10 ADL13849	Adl13849 Osteoarth
17	107.2	22.0	854	1 AAN91258	Aan91258 Nucleotid
18	107.2	22.0	854	6 ABV69731	Abv69731 Prostate
19	107.2	22.0	854	6 ABV94158	Abv94158 Breast ca
20	107.2	22.0	854	8 ACC46906	Acc46906 Human pho
21	107.2	22.0	854	10 ADB75500	Adb75500 Prostate

22	107.2	22.0	854	10 ADL13846	Adl13846 Osteoarth
23	107.2	22.0	854	11 ADI131881	Adi131881 Human CDN
24	107.2	22.0	967	10 ADD18503	Add18503 Human pro
25	107.2	22.0	997	12 AAL52397	Aal52397 Human sec
26	107.2	22.0	997	12 ADN03977	Adn03977 Antipsori
27	107.2	22.0	1028	10 ADL13851	Adl13851 Osteoarth
28	107.2	22.0	1076	3 AAF15635	Aaf15635 Human pro
29	107.2	22.0	1116	2 AAZ41274	Aaz41274 Human nor
30	107.2	22.0	1156	12 ADO22611	Ado22611 Human sof
31	105.6	21.7	479	2 AAQ26372	Aaq26372 PLA2 CDNA
32	101.4	20.8	375	10 ADF51390	Adf51390 Mutant hu
33	101.4	20.8	375	10 ADA61977	Ada61977 Human CDN
34	100	20.5	372	1 AAN97209	Aan97209 DNA enccd
35	99.8	20.5	1016	6 ABL59517	AbL59517 Human pho
36	99.8	20.5	1016	10 ADB31301	Adb31301 Testoster
37	99.8	20.5	1016	10 ACC82789	Acc82789 Human pho
38	99.8	20.5	1399	12 ADH13785	Adh13785 Human ENZ
39	98.2	20.2	1014	2 AAQ81138	Aaq81138 HPLA2-10
40	89.4	18.4	854	4 AAH23112	Aah23112 Osteoarth
41	86	17.7	778	8 ACC46913	Acc46913 Mouse pho
42	86	17.7	810	2 AAT48835	Aat48835 Mouse PLA
43	85.8	17.6	1828	2 AAQ81137	Aaq81137 RPLA2-10
44	85.4	17.5	592	3 AAS53269	Aas53269 Human pho
45	85.4	17.5	878	3 AAA60878	Aaa60878 Human sec

ALIGNMENTS

RESULT 1
AAAF77401
ID AAF77401 standard; CDNA; 487 BP.
XX AC AAF77401;
XX 12-JUN-2001 (first entry)
XX Human phospholipase A2 (PLA2) cDNA.
KW Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnary;
KW antiinflammatory; tranquiliser; antiasthmatic; antiallergic; trauma;
KW arthritic; antiasthmatic; septic shock; pancreatitis;
KW adult respiratory distress syndrome; ARDS; bronchial asthma; human;
KW allergic rhinitis; rheumatoid arthritis; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 59..487
FT /*tag= a
FT /product= "PLA2"
FT /note= "Phospholipase A2"
FT sig_peptide 59..115
FT /*tag= b
FT /label= Signal_peptide
FT mat_peptide 116..484
FT /*tag= c
FT /label= Mature_PLA2
FT /note= "Mature phospholipase A2"
XX WO200121775-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-JP006344.
XX 21-SEP-1999; 99JP-00266616.
XX (SHIO) SHIONOGI & CO LTD.
XX Ishizaki J, Suzuki N, Hanaeaki K;
XX WPI; 2001-290432/30.

```
DR P-PSDB; AAB81022.
XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
PT and screening drug candidates for treating associated diseases e.g.
PT septic shock, adult respiratory distress syndrome and rheumatoid
PT arthritis.
XX
XX Claim 5; Page 45-46; 50pp; Japanese.
XX
XX This invention relates to human secretory phospholipase A2 (PLA2) protein
XX and the gene encoding it. Inhibitors of phospholipase A2 have
XX antibacterial, immunosuppressive, antiinflammatory, tranquiliser,
XX vulnary, antiasthmatic, antiallergic, antirheumatic, and antiarthritic
XX activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
XX the diagnosis of PLA2 associated diseases e.g. septic shock, adult
XX respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
XX allergic rhinitis and rheumatoid arthritis. The present sequence
XX represents human cDNA encoding PLA2
XX
SQ Sequence 487 BP; 85 A; 157 C; 133 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 487; DB 5; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.1e-121; Indels 0; Gaps 0;
Matches 487; Conservative 0; Mismatches 0;

QY 1 CTGCTTTCTCTGCTGCTTTTATGCTCTCTTGTGCACTCCCTCCCGCAACCTGGAT 60
DB 1 CTGCTTTCTCTGCTGCTTTTATGCTCTCTTGTGCACTCCCTCCCGCAACCTGGAT 60

QY 61 GAAATCTCCCACTGCTGCTGCTTTTCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 GAAATCTCCCACTGCTGCTGCTTTTCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCT 120

QY 121 GTTTCAGTTTGGGTGATGATCGAGAGATGACAGGCAAGTCCGCTGAGTACACGA 180
DB 121 GTTTCAGTTTGGGTGATGATCGAGAGATGACAGGCAAGTCCGCTGAGTACACGA 180

QY 181 CTATGGCTGTTTACTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 CTATGGCTGTTTACTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 241 CTGCGACGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 CTGCGACGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

QY 301 GGAAAAGTATCTTTTCTGTCAGCGAACGTTGGCATTTTCTGCGCGGCAAGCACTCTG 360
DB 301 GGAAAAGTATCTTTTCTGTCAGCGAACGTTGGCATTTTCTGCGCGGCAAGCACTCTG 360

QY 361 CCAGGGCTGACCTGCGAGTGTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 CCAGGGCTGACCTGCGAGTGTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 CACCTACACCGCAAAATATGCCCATTAATCCCAAGCTGTGCAACCGGCGCCACCCGCC 480
DB 421 CACCTACACCGCAAAATATGCCCATTAATCCCAAGCTGTGCAACCGGCGCCACCCGCC 480

QY 481 CTGCTGA 487
DB 481 CTGCTGA 487

RESULT 2
ID AAA73130 standard; cDNA; 883 BP.
XX
XX AAA73130;
XX
XX 27-NOV-2000 (first entry)
XX
XX Mouse secretory type phospholipase A2 encoding cDNA SEQ ID NO:14.
XX
XX Mouse; secretory phospholipase A2; PLA2; screening; development;
```

```
inhibitor; ss.
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 166..594
XX FT /*tag= a
XX FT /product= "secretory type phospholipase A2"
XX FT 166..222
XX FT /*tag= b
XX FT 223..591
XX FT /*tag= c
XX
XX JP2000166568-A.
XX
XX 20-JUN-2000.
XX
XX 09-DEC-1998; 98JP-00349604.
XX
XX 09-DEC-1998; 98JP-00349604.
XX
XX (SHIO ) SHIONOGI & CO LTD.
XX
XX WPI: 2000-485554/43.
XX
XX P-PSDB; AAB12810.
XX
XX New gene encoding mouse secretory type phospholipase A2 (PLA2) for
XX screening for inhibitors of PLA2.
XX
XX Claim 5; Page 10-13; 15pp; Japanese.
XX
XX The present invention describes a mouse secretory type phospholipase A2
XX (PLA2) protein. The mouse secretory type PLA2-like protein can be used
XX for screening in the development of inhibitors against the function of
XX the protein. The present sequence encodes mouse secretory type PLA2
XX
XX Sequence 883 BP; 212 A; 277 C; 220 G; 174 T; 0 U; 0 Other;

Query Match 63.4%; Score 308.6; DB 3; Length 883;
Best Local Similarity 80.3%; Pred. No. 2.4e-73;
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 37 CCTCCCTTCCCGCAACCTGGGATGAAATCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCT 96
DB 144 CCCCCTGCTACTCTCCCGCAAGATGAAACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 203

QY 97 GGTGCTCTGTGTCACCGGGAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 156
DB 204 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 263

QY 157 CAAAGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 216
DB 264 AAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323

QY 217 GCCGCTGCAACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 276
DB 324 GCCAGTGGACGAGACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 383

QY 277 GAAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
DB 384 GAAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443

QY 337 TTTTCTGCGCGGCGGACCACTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
DB 444 CTTCTGTGCTGTAGAACGGCTTGCAGCGGATACCTGCGAGTGTGACAGAGAGCTGCTG 503

QY 397 CTTCTGCTTTCCCGCAACCTGGGACCTTACAAACGCAATATGCCCATTTATCCCAACAA 456
DB 504 TCTTTGCTTTCCCGCAACCTGAACTTACAAACGCAATATGCCCATTTATGCCCATTTAC 563

QY 457 GCTGTGACCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
DB 564 GCTGTGACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 594
```

RESULT 3

AAF77387

ID AAF77387 standard; cDNA; 883 BP.

XX AC

AAF77387;

XX DT

12-JUN-2001 (first entry)

XX DE

Murine cDNA encoding phospholipase A2 (PLA2).

XX KW

Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary;

XX KW

antiinflammatory; tranquiliser; antiasthmatic; antiallergic; trauma;

XX KW

antirheumatic; antiallergic; septic shock; pancreatitis; mouse;

XX KW

adult respiratory distress syndrome; ARDS; bronchial asthma;

XX KW

allergic rhinitis; rheumatoid arthritis; ss.

XX OS

Mus musculus.

XX FH

Key Location/Qualifiers

XX FT

166..594

XX FT

/*tag= a

XX FT

/product= "PLA2"

XX FT

/note= "Phospholipase A2"

XX FT

166..222

XX FT

/*tag= b

XX FT

/label= Signal_peptide

XX FT

mat_peptide

XX FT

223..591

XX FT

/*tag= c

XX FT

/label= Mature_PLA2

XX PN

WO200121775-A1.

XX PD

29-MAR-2001.

XX PF

18-SEP-2000; 2000WO-JP006344.

XX PR

21-SEP-1999; 99JP-00266616.

XX PA

(SHIO) SHIONOGI & CO LTD.

XX PI

Ishizaki J, Suzuki N, Hanasaki K;

XX DR

WPI; 2001-290432/30.

XX DR

P-PSDB; AAB81021.

XX PT

Human secretory phospholipase A2 and encoded gene, useful in diagnosis of

XX PT

and screening drug candidates for treating associated diseases e.g.

XX PT

septic shock, adult respiratory distress syndrome and rheumatoid

XX PT

arthritis.

XX PS

Example 3; Page 41-42; 50pp; Japanese.

XX CC

This invention relates to human secretory phospholipase A2 (PLA2) protein

XX CC

and the gene encoding it. Inhibitors of phospholipase A2 have

XX CC

antibacterial; immunosuppressive; antiinflammatory; tranquiliser;

XX CC

vulnerary; antiasthmatic; antiallergic; antirheumatic; and antiarthritic

XX CC

activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in

XX CC

the diagnosis of PLA2 associated diseases e.g. septic shock, adult

XX CC

respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,

XX CC

allergic rhinitis and rheumatoid arthritis. The present sequence

XX CC

represents cDNA encoding murine PLA2. The murine PLA2 gene sequence is

XX CC

used in the invention for the identification and characterisation of the

XX CC

human PLA2 gene

XX SQ

Sequence 883 BP; 212 A; 277 C; 220 G; 174 T; 0 U; 0 Other;

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

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Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

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Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

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Query Match

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Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

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Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

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Pred. NO. 2.4e-73;

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Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

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Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

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Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

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Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

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Query Match

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Matches 362; Conservative

0; Mismatches 89; Indels

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0; Length 883;

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37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

0; Gaps

0; Length 883;

Pred. NO. 2.4e-73;

37 CCTCCCTTCCCGCAACCTGGATGAATCTCCCACTGCTGTGTTCTTGCCTCCT 96

Query Match

Best Local Similarity

Matches 362; Conservative

0; Mismatches 89; Indels

Best Local Similarity 78.5%; Pred. No. 1.7e-41;
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

QY 146 AAGATGACAGGCAAGTCGCCCTGCAGTACAAAGCACTATGGCTGTACTGGCGCATCGGT 205
DB 5 AAGAGANGAGGGAACCTGCCCTGNAGTACAATNACTATGGCTGTATTGGCGGTGCGGT 64

QY 206 GGTCTCCACTGGCCGT-GGACCAAGTACTGCTGCTGCCAGCCGACGACTCTGCTA 264
DB 65 GGTCTCCACTGGCCGTGGGAGCAAGGATGGTGTGTCATGCCCATGACTGCTGCTA 124

QY 265 CGGGCGCTCGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTCTCTGTGAG 324
DB 125 TGGCCGCTGGAGANCTGGGCTGTGACCCCAAGCTGGAAAAGTACTCTTCTCTATCAC 184

QY 325 CGAACGTGGCATTTCTTGGCCGGGAGGACACCACTGCGAGCGGCTGACCTGGAGTGTGA 384
DB 185 TCGAGACAAATCTTCTGTGCTGGTAAACGGCTTGGCAGCGGCATACCTGCGAATGTGA 244

QY 385 CAAGAGGCTGCCCTGCTTTTGGCGGCAACCTGGGCACTTACAACCGCAATATGCCA 444
DB 245 CAA-AAACCGCTCTCTGCTTTGGCGCAACCTGAACTTACAACCGCAANTATGCCA 303

QY 445 TTATCCCAACAAGCTGT 461
DB 304 CTACCCCAACAAGCTGT 320

RESULT 5

ADL13850
ID AAF77374 standard; cDNA; 320 BP.

XX AAF77374;

DT 12-JUN-2001 (first entry)

DE Murine cDNA encoding phospholipase A2 (PLA2).

XX Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnery;
KW antiinflammatory; tranquilizer; antiallergic; antiallergic; trauma;
KW antirheumatic; antiarthritic; septic shock; pancreatitis; mouse;
KW adult respiratory distress syndrome; ARDS; bronchial asthma;
KW allergic rhinitis; rheumatoid arthritis; ss.

OS Mus musculus.

XX WO200121775-A1.

XX 29-MAR-2001.

XX 18-SEP-2000; 2000WO-JP006344.

XX 21-SEP-1999; 99JP-00266616.

XX (SHIO) SHIONOGI & CO LTD.

XX Ishizaki J, Suzuki N, Hanasaki K;

XX WPI; 2001-290432/30.

XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
PT and screening drug candidates for treating associated diseases e.g.
PT septic shock, adult respiratory distress syndrome and rheumatoid
PT arthritis.

XX Example 1; Page 38; 50pp; Japanese.

XX This invention relates to human secretory phospholipase A2 (PLA2) protein
CC and the gene encoding it. Inhibitors of phospholipase A2 have
CC antibacterial; immunosuppressive; antiinflammatory; tranquilizer;
CC vulnery; antiallergic; antirheumatic; and antiarthritic
CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult

CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
CC allergic rhinitis and rheumatoid arthritis. The present sequence
CC represents murine cDNA encoding PLA2 (EC.3.1.1.4). The murine sequence is
CC used in the invention for the identification and characterisation of the
CC human PLA2 gene

XX Sequence 320 BP; 78 A; 91 C; 76 G; 70 T; 0 U; 5 Other;

Query Match 39.1%; Score 190.4; DB 5; Length 320;

Best Local Similarity 78.5%; Pred. No. 1.7e-41;
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

QY 146 AAGATGACAGGCAAGTCGCCCTGCAGTACAAAGCACTATGGCTGTACTGGCGCATCGGT 205

DB 5 AAGAGANGAGGGAACCTGCCCTGNAGTACAATNACTATGGCTGTATTGGCGGTGCGGT 64

QY 206 GGTCTCCACTGGCCGT-GGACCAAGTACTGCTGCTGCCAGCCGACGACTCTGCTA 264

DB 65 GGTCTCCACTGGCCGTGGGAGCAAGGATGGTGTGTCATGCCCATGACTGCTGCTA 124

QY 265 CGGGCGCTCGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTCTCTGTGAG 324

DB 125 TGGCCGCTGGAGANCTGGGCTGTGACCCCAAGCTGGAAAAGTACTCTTCTCTATCAC 184

QY 325 CGAACGTGGCATTTCTTGGCCGGGAGGACACCACTGCGAGCGGCTGACCTGGAGTGTGA 384

DB 185 TCGAGACAAATCTTCTGTGCTGGTAAACGGCTTGGCAGCGGCATACCTGCGAATGTGA 244

QY 385 CAAGAGGCTGCCCTGCTTTTGGCGGCAACCTGGGCACTTACAACCGCAATATGCCA 444

DB 245 CAA-AAACCGCTCTCTGCTTTGGCGCAACCTGAACTTACAACCGCAANTATGCCA 303

QY 445 TTATCCCAACAAGCTGT 461

DB 304 CTACCCCAACAAGCTGT 320

RESULT 6

ADL13850
ID ADL13850 standard; DNA; 180550 BP.

XX ADL13850;

DT 06-MAY-2004 (first entry)

XX Osteoarthritis-associated polymorphic nucleotide #382.

XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW joint space narrowing; osteophyte development; joint pain;
KW osteoarthritis; SNP; single nucleotide polymorphism.

XX Homo sapiens.

XX WO2003054166-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-US041225.

XX 20-DEC-2001; 2001US-0342603P.

XX (INCY-) INCYTE GENOMICS INC.

XX Jones KA, Schafer A;

XX WPI; 2003-559141/52.

XX Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding
PT a protein.

XX Disclosure; SEQ ID NO 382; 297pp; English.

Db 594 TGTGTGAGTGTGATAGGCTGTGCGACCTGTTTGTGTAAGAAAGAGACCTACAATA 653
 QY 432 GCAAAATATGCCATTATCCACACAGCTGTGACCGGGCCACCGGCGCTGCTGA 487
 Db 654 AAAAGTACCAGTACTATTCCATAAAMACTGCAGAGGGAGACCCCTCGTTGCTGA 709
 RESULT 10
 ID ABV29244 standard; cDNA; 1160 BP.
 XX
 AC ABV29244;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 29235.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW Pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 6238; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6213); of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the aggressiveness or indolence of prostate cancer in a patient
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 1160 BP; 319 A; 314 C; 280 G; 238 T; 0 U; 9 Other;
 Query Match 22.3%; Score 108.8; DB 5; Length 1160;
 Best Local Similarity 55.5%; Pred. No. 3.1e-19;
 Matches 231; Conservative 0; Mismatches 182; Indels 3; Gaps 1;
 QY 75 TCGTGGTTCCTTTGGCTCTCTGGTGTGTCACCGGAACTGTTGAGTTGGGG 134
 Db 294 TGGCAGTGCATGATCTTTGGCTTACTGTCAGGCGCCATGGGAATTTGGTAATTCACA 353
 QY 135 TGATGATCGAAGATGACAGCGAAG---TCGGCCCTGCATACAGACTATCGCTT 191

Db 354 GAATGATCAAGTTGACACAGGAAAGGAGCGCACTCAGTTATGGCTTCTATGGGTGCC 413
 QY 192 ACTCGCGCATCGTGGCTCCCACTGGCGCGTGGACACAGACTGCTGTGTGTCACGCC 251
 Db 414 ACTGTGCGGTGGTGGGAGAGGATCCCCCAAGGATGCAACGGATCGCTGTGTGTCATC 473
 QY 252 ACGACTGCTGTCTACGGCGCTCTGAGAAAGCTGGGCTGTGAGCCCAAACTGGAAGTATC 311
 Db 474 ATGACTGTGCTACAAACGCTCTGGAGAAACGTGATGTGGACCAAAATTTCTGAGCTACA 533
 QY 312 TTTTCTCTGTACGGAACGTGGCATTTTCTGGCGCGGACGACCACTGCCAGCGGTGA 371
 Db 534 AGTTAGCAACTCGGGAGCAGAAATCACCTGTGTCAAAAACAGGACTCCTGTGAGAACTCAAC 593
 QY 372 CCTGCGAGTGTGCAAGAGGGCTGCCCTCTGCTTTGGCCGCAACCTGGGACCTACAACC 431
 Db 594 TGTGTGAGTGTGATAGGCTGTGCCACCTGTTTGTGTAAGAAACAGACGACCTACAATA 653
 QY 432 GCAAAATATGCCATTATCCCAACAAAGCTGTGACCGGGCCACCGGCGCTGCTGA 487
 Db 654 AAAAGTACCAGTACTATTCCATAAAMACTGCAGAGGGAGACCCCTCGTTGCTGA 709
 RESULT 11
 ID ABV23388 standard; cDNA; 1160 BP.
 XX
 AC ABV23388;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 23379.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW Pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 4251; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the aggressiveness or indolence of prostate cancer in a patient;
 CC (g) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)

CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1160 BP; 319 A; 314 C; 280 G; 238 T; 0 U; 9 Other;
Query Match 22.3%; Score 108.8; DB 5; Length 1160;
Best Local Similarity 55.5%; Pred. No. 3.1e-19;
Matches 231; Conservative 0; Mismatches 182; Indels 3; Gaps 1;
QY 75 TCGTGGTCTCTTGGCTCCCTGGCTCTGGTCAACGGGACCTGCTTCAAGTTGGGG 134
DB 294 TGGCAGTGATCATGATCTTTGGCTACTGAGCCCACTGGGAATTTGGTGAATTCACCA 353
QY 135 TGATGATCGAAGATGACAGGCAAG---TCGGCCCTGCAGTACACGACTATGGCTGTT 191
DB 354 GAATGATCAAGTTGACGACAGGAAGGAGCGCACTCAGTTATGGCTTCTATGGCTGCC 413
QY 192 ACTGGGCTATCGGTGGCTCCCACTGGCGGTGGACGACTGACTGTGCTGCCAGGCC 251
DB 414 ACTGTGGCTGGTGGCAGAGGATCCCAAGGATGCAACGGATCGCTGCTGTGCACTC 473
QY 252 AGCACTGCTGACAGAGGCTGCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAATATC 311
DB 474 ATGACTGTTCTACAACTGCTGGAGAACTGGGATGTGGACCAAAATTTCTGAGCTACA 533
QY 312 TTTTCTCTGTCAGGAACTGGGCAATTTCTGCGCGGAGGACCACTCTGCGCACTACAAC 371
DB 534 AGTTAGCAACTCGGGGAGCAGAACTACCTGTGCAAAAACAGGACTCCTGCAGAGTCAAC 593
QY 372 CCTGCGAGTGTGACAGAGGCTGCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAATATC 431
DB 594 TGTGTGAGTGTGATAGGCTGCTGCCACCTGTTTGTAGAAAACAGACGACCTACAATA 653
QY 432 GCAAAATATGCCATTTATCCCAACAGCTGTGACCGGGCCACCCCGCTGCTGA 487
DB 654 AAAAGTACCAGTACTATTCCCAATAAACACTGACAGAGGAGGACCCCTCGTTGCTGA 709
RESULT 12
ABV2535 standard; cDNA; 1160 BP.
XX AC ABV2535;
XX DE 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 25526.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX PI WPI; 2001-662795/76.
XX DR Novel isolated nucleic acid molecule associated with cancerous state of
XX PT

PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5084-5084; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1160 BP; 319 A; 314 C; 280 G; 238 T; 0 U; 9 Other;
Query Match 22.3%; Score 108.8; DB 5; Length 1160;
Best Local Similarity 55.5%; Pred. No. 3.1e-19;
Matches 231; Conservative 0; Mismatches 182; Indels 3; Gaps 1;
QY 75 TCGTGGTCTCTTGGCTCCCTGGCTCTGGTCAACGGGACCTGCTTCAAGTTGGGG 134
DB 294 TGGCAGTGATCATGATCTTTGGCTACTGAGCCCACTGGGAATTTGGTGAATTCACCA 353
QY 135 TGATGATCGAAGATGACAGGCAAG---TCGGCCCTGCAGTACACGACTATGGCTGTT 191
DB 354 GAATGATCAAGTTGACGACAGGAAGGAGCGCACTCAGTTATGGCTTCTATGGCTGCC 413
QY 192 ACTGGGCTATCGGTGGCTCCCACTGGCGGTGGACGACTGACTGTGCTGCCAGGCC 251
DB 414 ACTGTGGCTGGTGGCAGAGGATCCCAAGGATGCAACGGATCGCTGCTGTGCACTC 473
QY 252 AGCACTGCTGCTACGGGCGTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAATATC 311
DB 474 ATGACTGTTCTACAACTGCTGGAGAACTGGGATGTGGACCAAAATTTCTGAGCTACA 533
QY 312 TTTTCTCTGTCAGGAACTGGGCAATTTCTGCGCGGAGGACCACTCTGCGCACTACAAC 371
DB 534 AGTTAGCAACTCGGGGAGCAGAACTACCTGTGCAAAAACAGGACTCCTGCAGAGTCAAC 593
QY 372 CCTGCGAGTGTGACAGAGGCTGCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAATATC 431
DB 594 TGTGTGAGTGTGATAGGCTGCTGCCACCTGTTTGTAGAAAACAGACGACCTACAATA 653
QY 432 GCAAAATATGCCATTTATCCCAACAGCTGTGACCGGGCCACCCCGCTGCTGA 487
DB 654 AAAAGTACCAGTACTATTCCCAATAAACACTGACAGAGGAGGACCCCTCGTTGCTGA 709
RESULT 13
ABV29221 standard; cDNA; 1160 BP.
XX ID ABV29221
XX AC ABV29221;
XX DE 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 29212.
XX DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 05:01:22 ; Search time 59 Seconds
(without alignments)
5867.020 Million cell updates/sec

Title: US-10-088-092a-29

Perfect score: 487

Sequence: 1 cgcgtttcttctgtgcctt.....ggcccccacccgcctgtgta 487

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:**

- 1: /cgn2_6/prodata/1/ina/5A COMB.seq:**
- 2: /cgn2_6/prodata/1/ina/5B COMB.seq:**
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:**
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq:**
- 5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:**
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107.2	22.0	854	4	US-09-023-655-1207
2	105.6	21.7	479	1	US-08-186-895-9
3	101.4	20.8	375	4	US-09-740-569-1
4	101.4	20.8	375	4	US-10-255-576-1
5	99.8	20.5	1016	4	US-09-220-132-17
6	98.2	20.2	1014	2	US-08-888-497-31
7	98.2	20.2	1014	3	US-09-362-230-31
8	98.2	20.2	1014	5	PCT-US94-07926-31
9	85.8	17.6	1828	2	US-08-888-497-29
10	85.8	17.6	1828	3	US-09-362-230-29
11	85.8	17.6	1828	5	PCT-US94-07926-29
12	85.4	17.5	878	4	US-09-855-486-26
13	64.8	13.3	4325	2	US-08-888-497-21
14	64.8	13.3	4325	3	US-09-362-230-21
15	64.8	13.3	4325	5	PCT-US94-07926-21
16	61.4	12.6	742	3	US-08-966-317-2
17	61.4	12.6	742	3	US-09-489-770-2
18	60.8	12.5	501	4	US-09-855-486-13
19	60.8	12.5	1233	4	US-09-855-486-13
20	60.2	12.4	496	4	US-10-140-002-533
21	58.4	12.0	562	4	US-09-023-655-1200
22	41.2	8.5	441	4	US-09-252-991A-14930
23	41.2	8.5	657	4	US-09-252-991A-14930
24	40.4	8.3	1686	4	US-09-252-991A-15047
25	40.4	8.3	1761	4	US-09-252-991A-5746
26	40.4	8.3	1890	4	US-09-252-991A-5762
27	38.8	8.0	1491	4	US-09-331-733-21

c

Query Match 22.0%; Score 107.2; DB 4; Length 854;

28	38.4	7.9	1338	1	US-08-307-444A-8	Sequence 8, Appli
29	38.4	7.9	1338	1	US-08-587-389-8	Sequence 8, Appli
30	38.4	7.9	1368	1	US-08-307-444A-7	Sequence 7, Appli
31	38.4	7.9	1368	1	US-08-587-389-7	Sequence 7, Appli
32	38.4	7.9	1425	1	US-08-307-444A-6	Sequence 6, Appli
33	38.4	7.9	1425	1	US-08-587-389-6	Sequence 6, Appli
34	38	7.8	15328	2	US-08-888-497-33	Sequence 33, Appli
35	38	7.8	15328	3	US-09-362-230-33	Sequence 33, Appli
36	38	7.8	15328	5	PCT-US94-07926-33	Sequence 33, Appli
37	37.8	7.8	1425	1	US-08-307-444A-23	Sequence 23, Appli
38	37.8	7.8	1425	1	US-08-587-389-23	Sequence 23, Appli
39	37.2	7.6	825	1	US-08-312-870-6	Sequence 6, Appli
40	37.2	7.6	1428	1	US-08-014-723-3	Sequence 3, Appli
41	37.2	7.6	1428	1	US-08-014-723-4	Sequence 4, Appli
42	37.2	7.6	1428	1	US-08-110-011A-3	Sequence 3, Appli
43	37.2	7.6	1428	1	US-08-110-011A-4	Sequence 4, Appli
44	37.2	7.6	1491	1	US-08-312-870-2	Sequence 2, Appli
45	37.2	7.6	1680	1	US-08-014-723-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-023-655-1207
; Sequence 1207, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1207:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENE BANK
; CLONE: g190888
; US-09-023-655-1207

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 233..643
US-08-888-497-29

Query Match 17.6%; Score 85.8; DB 2; Length 1828;
Best Local Similarity 52.9%; Pred. No. 1.8e-15;
Matches 208; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 82 GTTCCTTTGCCCTCGCTGGTGGCTCTGTCACCGGGAACCTGGTTTCAGTTTGGGGTGATGAT 141
Db 259 GTTCCTGGCTTGAGTGTGCTGCTGAGTCCAGGGGGCTGTGTAAGTGAAGTCCATGAT 318
Qy 142 CGAGAGATGACAGGCAAGTCCGCTTCAGTACAA---CGACTATGGCTGTACTGCGG 198
Db 319 TGAGAAGGTGACTGGGAAGAAATCCGTAAAGAACTATGGCTTCTACGGCTGTCTGTGG 378
Qy 199 CATCGTGGCTCCCACTGGCGGCTGGACAGACTGCTGGTGTGCGACGCCACGACTG 258
Db 379 CTGGGGCGGCACGGGACCCCTTAAGATGACATGTTGGTGTGCTGTGGATGACACCG 438
Qy 259 CTGCTACGGGCGCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTTCT 318
Db 439 TTGTTATGGGCTACTGGAGGAGAAACACTGTGCATCCGAGCCAGTCTATGACTACAG 498
Qy 319 TGTACGGAAGCTGGGCAATTTTCTGGCCGCGACGAGACACCTGCGAGGGCTGACCTGCGA 378
Db 499 ATTCACACAGGACTTAGTCACTCTCGAACAACGACTCTCTGTCAGTGGCTTTGTGC 558
Qy 379 GTGTGACAAGAGGCTGCCCTCTGCTTCGCCCAACCTGGGCACTCTGAGGAGAACTCTGGAGTTACACCGTCTTTA 618
Db 559 TTGTGACCGGAAGCTGTCTACTGCTGAGGAGAACTCTGGAGTTACACCGTCTTTA 618
Qy 439 TGCCCATTTATCCCAACAAAGTGTGACCGGGCC 471
Db 619 CCAGTATTACCCCAACTTCTCTGCTAAATGTCC 651

RESULT 11
PCT-US94-07926-29
Sequence 29, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruten, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 233..643
US-08-888-497-29

Query Match 17.6%; Score 85.8; DB 2; Length 1828;
Best Local Similarity 52.9%; Pred. No. 1.8e-15;
Matches 208; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 82 GTTCCTTTGCCCTCGCTGGTGGCTCTGTCACCGGGAACCTGGTTTCAGTTTGGGGTGATGAT 141
Db 259 GTTCCTGGCTTGAGTGTGCTGCTGAGTCCAGGGGGCTGTGTAAGTGAAGTCCATGAT 318
Qy 142 CGAGAGATGACAGGCAAGTCCGCTTCAGTACAA---CGACTATGGCTGTACTGCGG 198
Db 319 TGAGAAGGTGACTGGGAAGAAATCCGTAAAGAACTATGGCTTCTACGGCTGTCTGTGG 378
Qy 199 CATCGTGGCTCCCACTGGCGGCTGGACAGACTGCTGGTGTGCGACGCCACGACTG 258
Db 379 CTGGGGCGGCACGGGACCCCTTAAGATGACATGTTGGTGTGCTGTGGATGACACCG 438
Qy 259 CTGCTACGGGCGCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTTCT 318
Db 439 TTGTTATGGGCTACTGGAGGAGAAACACTGTGCCATCCGACCCAGTCTATGACTACAG 498
Qy 319 TGTACGGAAGCTGGGCAATTTTCTGGCCGCGACGAGACACCTGCGAGGGCTGACCTGCGA 378
Db 499 ATTCACACAGGACTTAGTCACTCTCGAACAACGACTCTCTGTCAGTGGCTTTGTGC 558
Qy 379 GTGTGACAAGAGGCTGCCCTCTGCTTCGCCCAACCTGGGCACTCTGAGGAGAACTCTGGAGTTACACCGTCTTTA 618
Db 559 TTGTGACCGGAAGCTGTCTACTGCTGAGGAGAACTCTGAGTTACACCGTCTTTA 618
Qy 439 TGCCCATTTATCCCAACAAAGTGTGACCGGGCC 471
Db 619 CCAGTATTACCCCAACTTCTCTGCTAAATGTCC 651

RESULT 10
US-09-362-230-29
Sequence 29, Application US/09362230
Patent No. 6352849
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruten, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 233..643
PCT-US94-07926-29

Query Match 17.6%; Score 85.8; DB 5; Length 1828;
Best Local Similarity 52.9%; Pred. No. 1.8e-15;
Matches 208; Conservative 0; Mismatches 182; Indels 3; Gaps 1;
QY 82 GTTCCTTTCCCTGCTGGTGGCTCTGGTCCACCGGGAACCTGGTTAGTTTGGGGTATCAT 141
DB 259 GTTCTGGTTCGAGTGTGCTGCTGAGTCCAGGCGGCTGTAGAACTGAAGTCCATGAT 318
QY 142 CGAGAAGATGACAGGCAAGTCCGCTCGAGTACAA---CGACTATGCTGTACTGCGG 198
DB 319 TGAGAAGGTGACTGGGAAGATCCGTAAGAACTATGGCTTCTACGGCTGCTACTGTGG 378
QY 199 CATCGTGGTCCACTGCGGTGGACGAGTCACTGCTGCTGCCAGCCGACGACTG 258
DB 379 CTGGGCGGCCACCGGACCCCTAAGATGGCACTGATTGGTCTGCTGGATGACGACCG 438
QY 259 CTGCTACGGCGCTCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAGAAATATCTTTC 318
DB 439 TTGTTATGGCTACTGGAGGAACAACCTGTCCATCCGACCCAGTCTATGACTACAG 498
QY 319 TGTACGGAACGTGGCATTTTCTGGCGCGGAGGACCACTGCCAGCGGCTGACCTGCGA 378
DB 499 ATTACACAGGACTTAGTTCATCTCGGAACACGACTCCTTCTGTCAGTGAGGCTTTGTGC 558
QY 379 GTGTGACAGAGGCTGCCCTCTGTTTCGCGCAACCTGGGCACTACAAACGCAATA 438
DB 559 TTGTGACCGAGCTGCTCTGCTGCTGAGGAAACCTCTGGAGTTACACCGCTTTA 618
QY 439 TGCCCATTTACCAACAACTGTGACCGGGCC 471
DB 619 CCAATATTACCCCAACTTCTCTGCTGAATGTC 651

RESULT 12
US-09-856-486-26
Sequence 26, Application US/09856486
Patent No. 6756219
GENERAL INFORMATION:
APPLICANT: ISHIZAKI, JUN
APPLICANT: SUZUKI, NORIKO
APPLICANT: HANASAKI, KOHJI
TITLE OF INVENTION: A HUMAN SECRETORY TYPE PHOSPHOLIPASE A2

FILE REFERENCE: 209308US-4346-4346-0-PCT
CURRENT APPLICATION NUMBER: US/09/856,486
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: JP10/349608
PRIOR FILING DATE: 1998-12-09
PRIOR APPLICATION NUMBER: PCT/JP99/06844
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent in version 3.1
SEQ ID NO 26
LENGTH: 878
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(463)
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: (89)..()
OTHER INFORMATION:
US-09-856-486-26

Query Match 17.5%; Score 85.4; DB 4; Length 878;
Best Local Similarity 54.3%; Pred. No. 1.7e-15;
Matches 195; Conservative 0; Mismatches 161; Indels 3; Gaps 1;
QY 74 GTGCTGGTGTTCCTTTGCTCCCTGGTGGCTCTGGTCCACCGGGAACCTGGTTCAAGTTGGG 133
DB 50 GGGCTGGTGTGATGGTGTGATTTCAATCCAGGGCGGATCCTGAACCTGAACAAG 109
QY 134 GTGATGATCGAGAAGATGACAGCAAGTCCGCCCTGCAGTACAACTATGCTGTATC 193
DB 110 ATGCTCAAGCAAGTACTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTAC 169
QY 194 TGGCGCATCGTGGTCTCCACTGGCGGTGGACAGACTGACTGGTGTGCCACGCCAC 253
DB 170 TGGGACTAGTGGCAGAGCCCAACCAAGATGCCACGAGCTGGTGTGCCAGACCCAT 229
QY 254 GACTGCTGTACGGGCTCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAAGTATCTT 313
DB 230 GACTGTGCTATGACCACCTGAAGACCCAGGGTGGGCAATCTACAAGGACTATTACAG 289
QY 314 TTCTCTGACGCAACCGTGGCATTTTCTGCGCGGCA---GGACCACTGCCAGCGGCTG 370
DB 290 TACAACCTTTCCAGGGGAACATCCACTGCTCTGACAAGGAAGCTGGTGTGAGCAGCAG 349
QY 371 ACTGCGAGTGTGACAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGSCACCTACAA 429
DB 350 CTGTGCTCTGTGACAGAGGAGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACCA 408

RESULT 13
US-08-888-497-21
Sequence 21, Application US/08888497
Patent No. 5972677
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: US/08/888,497
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: US/08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 722..1195
US-08-888-497-21

Query Match 13.3%; Score 64.8; DB 2; Length 4325;
Best Local Similarity 53.5%; Pred. No. 3.8e-09;
Matches 166; Conservative 0; Mismatches 132; Indels 12; Gaps 1;
QY 132 GGGTGTATCGAGAGATGACAGGCAAGTCGCGCTGCAGTACAAAGACTATGCTGT 191
DB 825 GGATGTCACACATCAGCGGCGCAGCGCTTCTTCTCTATTACGGATATGGCTGT 884
QY 192 ACTGCGGCATCGGTGCTCCACTGCGCGTGACAGACTGCTGCTGCCACGCC 251
DB 885 ACTGTGGCTTGGGGCCGAGGATCCCTGTGACGCCACAGACAGTGTCTGGCTC 944
QY 252 AGACTGCTGTACGGCGCTGAGAGAGCTGGAGAGCTGGAGCCAACTGGAAAGTATC 311
DB 945 ATGACTGTGTACCAACAGCTTAAGGAATATGGCTGCCAGCCCATCTTGAATGCTATC 1004
QY 312 TTTTCTCTGACGCAACGTGGCAATTTCTG-----CGCGCGCAGGACCACT 359
DB 1005 AGTTGCCATTGTCAACGGGACCGTGACCTGTGGATGCACCATGGTGGCTGTTGT 1064
QY 360 GCCAGCGGTGACCTCGAGTGTGACAAGAGGCTGCCCTCTGCTTTCCGCCAACCTGG 419
DB 1065 GCGGGCAGAAAGCCTGTGAGTGTGACAAACTGTGTACTGCTTCAAGGAGAACCTGG 1124
QY 420 GCACCTACAA 429
DB 1125 CCACCTACGA 1134

RESULT 14
US-09-362-230-21
Sequence 21, Application US/09362230
Patent No. 6352849
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US/08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 722..1195
US-09-362-230-21

Query Match 13.3%; Score 64.8; DB 3; Length 4325;
Best Local Similarity 53.5%; Pred. No. 3.8e-09;
Matches 166; Conservative 0; Mismatches 132; Indels 12; Gaps 1;
QY 132 GGGTGTATCGAGAGATGACAGGCAAGTCGCGCTGCAGTACAAAGACTATGCTGT 191
DB 825 GGATGTCACACATCAGCGGCGCAGCGCTTCTTCTCTATTACGGATATGGCTGT 884
QY 192 ACTGCGGCATCGGTGCTCCACTGCGCGTGACAGACTGCTGCTGCCACGCC 251
DB 885 ACTGTGGCTTGGGGCCGAGGATCCCTGTGACGCCACAGACAGTGTCTGGCTC 944
QY 252 AGACTGCTGTACGGCGCTGAGAGAGCTGGAGAGCTGGAGCCAACTGGAAAGTATC 311
DB 945 ATGACTGTGTCTACCAACAGCTTAAGGAATATGGCTGCCAGCCCATCTTGAATGCTATC 1004
QY 312 TTTTCTCTGACGCAACGTGGCAATTTCTG-----CGCGCGCAGGACCACT 359
DB 1005 AGTTGCCATTGTCAACGGGACCGTGACCTGTGGATGCACCATGGTGGCTGTTGT 1064
QY 360 GCCAGCGGTGACCTCGAGTGTGACAAGAGGCTGCCCTCTGCTTTCCGCCAACCTGG 419
DB 1065 GCGGGCAGAAAGCCTGTGAGTGTGACAAACTGTGTACTGCTTCAAGGAGAACCTGG 1124
QY 420 GCACCTACAA 429
DB 1125 CCACCTACGA 1134

RESULT 15
PCT-US94-07926-21
Sequence 21, Application PC/TUS9407926
GENERAL INFORMATION:

APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 722..1195
PCT-US94-07926-21

Query Match 13.3%; Score 64.8; DB 5; Length 4325;
Best Local Similarity 53.5%; Pred. No. 3.8e-09;
Matches 166; Conservative 0; Mismatches 132; Indels 12; Gaps 1;
QY 132 GGGTGATGATCGAGAGATGACAGGCAAGTCGGCCCTGCAGTACACAGACTATGGCTGTT 191
DB 825 GGATGGTCAAAACACATCACGGGGCGCGCCCTTCTCTCTATTACGGATATGGCTGCT 884
QY 192 ACTGGCGCATCGGTGGCTCCCACTGGCGGTGGACAGACTGCTGGTGTGCCACGCC 251
DB 885 ACTGTGGGCTGGGGGGCCGAGGGATCCCTGTGGAGCCACAGACAGTGTCTGGGCTC 944
QY 252 AGACTGTGTCTACGGGCGTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATC 311
DB 945 ATGACTGTGTCTACCAAGCTTAAAGGAATATGGCTGCCAGCCCATCTTGAATGCCTATC 1004
QY 312 TTTTCTCTGCAGCGAAGTGGCATTTCTG-----CGCGGCGAGGACCACT 359
DB 1005 AGTTTGCCATTTGTAACGGGACCGTGACCTGTGGATGACCATGGTGGCGGCTGCTTGT 1064
QY 360 GCCAGCGGCTGACCTGCGAGTGTGACAAGAGGGTGGCCCTCTGCTTTTCCCGCAACCTGG 419
DB 1065 GCGGGCAGAAAGCTGTGAGTGTGACAAACTGTCTGTCTGTCTCAAGGAGAACCTGG 1124
QY 420 GCACCTACAA 429
DB 1125 CCACCTACGA 1134

Search completed: November 13, 2004, 06:11:26
Job time : 60 secs

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1	107.2	22.0	854	9	US-09-969-708-597	Sequence 597, Appl
2	107.2	23.0	854	10	US-09-965-866-3	Sequence 3, Appl
3	107.2	23.0	854	15	US-10-305-823-324	Sequence 124, Appl
4	107.2	22.0	854	15	US-10-302-524-1758	Sequence 1758, Appl
5	107.2	22.0	854	15	US-10-007-526A-1	Sequence 149, Appl
6	107.2	22.0	854	15	US-10-072-118-465	Sequence 465, Appl
7	107.2	22.0	854	16	US-10-342-887-465	Sequence 465, Appl
8	107.2	22.0	854	16	US-10-641-643-1207	Sequence 1207, Appl
9	107.2	22.0	967	15	US-10-210-120-75	Sequence 75, Appl
10	107.2	22.0	1076	9	US-09-925-300-70	Sequence 70, Appl
11	101.4	20.8	375	9	US-09-740-569-1	Sequence 1, Appl
12	101.4	20.8	375	15	US-10-255-576-1	Sequence 1, Appl

Db 215 GAATGATCAAGTTGACGACAGGAAAGGAGCCGCACTCAGTTATGGCTTCTACGGCTGCC 274
QY 192 ACTGGGCAATCGGTGGCTCCCACTGGCGGTGGACCACTGACTGCTGGTCCACGGCC 251
Db 275 ACTGTGGCGTGGTGGCAGAGGATCCCCAAGGATGCAACGGATCGCTGTGTCACTC 334
QY 252 AGCACTGCTGCTACGGCGCTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAGATATC 311
Db 335 ATGACTGTTGCTACAAAGCTCTGGAGAACGTGGATGGCACCACAAATTTCTGAGCTACA 394
QY 312 TTTTCTCTCTACGCGAACCTGGCAATTTCTGCGCGGAGGACCACTGCGAGCGGCTGA 371
Db 395 AGTTTAGCAACTCGGGGAGCAGAAATCACCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 454
QY 372 CTGCGAGTGTGACAGAGGGCTGCCTCTGCTTTGCGCGCAACTGGCGCACTTACAACC 431
Db 455 TGTGTGAGTGTGATAGGCTGTGTCACCTGTTTGTAGAAACAGACGACCTACATA 514
QY 432 GCAATATGCCATTATCCCAACAGCTGTGACCGGGCCCAACCGCCGCTGCTGA 487
Db 515 AAAAGTACCAGTACTATTCCATAAACAAGTGTGAGAGGAGGACCCCTGTTGCTGA 570

RESULT 2
US-09-865-866-3
; Sequence 3, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 3
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(570)
US-09-865-866-3

Query Match 22.0%; Score 107.2; DB 10; Length 854;
Best Local Similarity 55.3%; Pred. No. 2.1e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGTGTGTTCTCTTTCCTCTGCTGGTCTGCTCAGCCGGGAACTGGTTCAGTTTGGGG 134
Db 155 TGGCAGTGATCATGATCTTTGGCCTACTGAGGCCCATGGGAATTTGGTGAATTTCCACA 214
QY 135 TGATGATCGAGAGATGACAGGCAAG---TCCGCCCTGCAGTACACGACTATGGCTGTT 191
Db 215 GAATGATCAAGTTGACGACAGGAAAGGAGCCCACTCAGTTATGGCTTCTACGGTGC 274
QY 192 ACTGCGGCATCGGTGCTCCCACTGCGCGGTGGACAGACTGACTGGTCTGCCACGCC 251
Db 275 ACTGTGGCTGGTGGGAGAGGATCCCCAAGGATGCAACGGATCGCTGTGTCACTC 334
QY 252 ACAGCTGCTGCTACGGCGCTCTGAGAGCTGGGCTGTGAGCCCAAACTGGAAGATATC 311
Db 335 ATGACTGTTGCTACAAAGCTCTGGAGAACGTGGATGGCACCACAAATTTCTGAGCTACA 394
QY 312 TTTTCTCTGTACGCAACGTGGCAATTTCTGCGCGGAGGACCACTGCGCAGCGGCTGA 371
Db 395 AGTTTAGCAACTCGGGGAGCAGAAATCACCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 454
QY 372 CTGCGAGTGTGACAGAGGGCTGCCTCTGCTTTGCGCGCAACTGGCGCACTTACAACC 431
Db 455 TGTGTGAGTGTGATAGGCTGTGTCACCTGTTTGTAGAAACAGACGACCTACATA 514
QY 432 GCAATATGCCATTATCCCAACAGCTGTGACCGGGCCCAACCGCCGCTGCTGA 487

Db 515 AAAAGTACCAGTACTATTCCATAAACAAGTGTGAGAGGAGGACCCCTGTTGCTGA 570

RESULT 3
US-10-205-823-324
; Sequence 324, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-324

Query Match 22.0%; Score 107.2; DB 15; Length 854;
Best Local Similarity 55.3%; Pred. No. 2.1e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGTGTGTTCTCTTTCCTCTGCTGGTCTGCTCAGCCGGGAACTGGTTCAGTTTGGGG 134
Db 155 TGGCAGTGATCATGATCTTTGGCCTACTGAGGCCCATGGGAATTTGGTGAATTTCCACA 214
QY 135 TGATGATCGAGAGATGACAGGCAAG---TCCGCCCTGCAGTACACGACTATGGCTGTT 191
Db 215 GAATGATCAAGTTGACGACAGGAAAGGAGCCCACTCAGTTATGGCTTCTACGGTGC 274
QY 192 ACTGCGGCATCGGTGCTCCCACTGCGCGGTGGACAGACTGACTGGTCTGCCACGCC 251
Db 275 ACTGTGGCTGGTGGGAGAGGATCCCCAAGGATGCAACGGATCGCTGTGTCACTC 334
QY 252 ACAGCTGCTGCTACGGCGCTCTGAGAGCTGGGCTGTGAGCCCAAACTGGAAGATATC 311
Db 335 ATGACTGTTGCTACAAAGCTCTGGAGAACGTGGATGGCACCACAAATTTCTGAGCTACA 394
QY 312 TTTTCTCTGTACGCAACGTGGCAATTTCTGCGCGGAGGACCACTGCGCAGCGGCTGA 371
Db 395 AGTTTAGCAACTCGGGGAGCAGAAATCACCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 454
QY 372 CTGCGAGTGTGACAGAGGGCTGCCTCTGCTTTGCGCGCAACTGGCGCACTTACAACC 431
Db 455 TGTGTGAGTGTGATAGGCTGTGTCACCTGTTTGTAGAAACAGACGACCTACATA 514
QY 432 GCAATATGCCATTATCCCAACAGCTGTGACCGGGCCCAACCGCCGCTGCTGA 487

Db 515 AAAAGTACCAAGTACTATTCCAAATAAACACTGCAGAGGGAGCACCCCTCGTTGCTGA 570

RESULT 4

US-10-102-524-1758

; Sequence 1758, Application US/10102524

; Publication No. US20030109434A1

; GENERAL INFORMATION:

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Gaiger, Alexander

; APPLICANT: Gordon, Brian

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER

; FILE REFERENCE: 210121.572

; CURRENT APPLICATION NUMBER: US/10/102,524

; CURRENT FILING DATE: 2002-03-19

; NUMBER OF SEQ ID NOS: 1863

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 1758

; LENGTH: 854

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-102-524-1758

Query Match 22.0%; Score 107.2; DB 15; Length 854;

Best Local Similarity 55.3%; Pred. No. 2.1e-23;

Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGTCTGGTGTTCCTTTGGCTCTCTGGTGGCTCTGGTCCACGGGAACTGTGTTTCAGTTTGGGG 134

DB 155 TGGCAGTGAATCATGATCTTTGGCCCTACTGCAGGCCCATGGGAATTTGGTGAATTTCCACA 214

QY 135 TGAATGTCGAGAGATGACAGGCAAG---TCCGCCCTGCAGTACACGACTATGGCTGTT 191

DB 215 GAATGATCAAGTTTCAACACAGGAAGAACGCCCACTCAGTTATGGGTTTCTACGGCTGCC 274

QY 192 ACTGCGGCATCGTGGGTCCCACTGGCGGGTGGACAGACTGACTGGTGTGTCGCACGCC 251

DB 275 ACTGTGCGTGGTGGCAGAGGATCCCCCAAGGATGCAACGGATCGCTGTGTCACATC 334

QY 252 ACAGACTCTCTACGGCGGTCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAGTATC 311

DB 335 ATGACTGTGCTACAAACGTTCTGGAGAAACGTGGATGGCACCACAAATTTCTGAGCTACA 394

QY 312 TTTTCTCTGTGAGGCAAGTGGCATTTTTCGCGCGGCAGACACCTGCCAGCGGGTGA 371

DB 395 AGTTAGCAACTCGGGAGCAGAAATCACCTGTGTCAAAACAGGACTCTCTGCAGAGTCAAC 454

QY 372 CCTGCGAGTGTGACAAGAGGCGCTGCCCTCTGCTTTCCGCCCAACTGGGCACCTACAACC 431

DB 455 TGTGTGAGTGTGAATAGGCTGCTCCACCTGTTTGTAGAAAACAAGACGACCTACAATA 514

QY 432 GCMAATATGCCCATATCCCAACAGCTGTGACCGGGCCACCGCCCTGCTGA 487

DB 515 AAAAGTACCAAGTACTATTCCAAATAAACACTGCAGAGGGAGCACCCCTCGTTGCTGA 570

RESULT 5

US-10-007-926A-149

; Sequence 149, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIENBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

```

; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: phospholipase a2, group iia (platelets,
; synovial fluid) (PLA2G2A) gene.
US-10-007-926A-149

Query Match 22.0%; Score 107.2; DB 15; Length 854;
Best Local Similarity 55.3%; Pred. No. 2.1e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

Qy 75 TGCTGGTGTTCCTTTGCCTCCTGGTGGCTCTGGTCACCGGAACTCGTTTCAGTTTGGGG 134
Db 155 TGGCAGTGATCATGATCTTTTGGCTACTGAGGCCCATGGGAATTTGGTGNATTTCCACA 214
Qy 135 TGATGATCGAGAAGATGACAGGCAAG---TCCGCCCTGCAGTACAAAGCATATCGCTGTT 191
Db 215 GAATGATCAAGTTGACGACAGGAAGAACGCCGACCTCAGTTATGGCTTCTACGGCTGCC 274
Qy 192 ACTGGCGCATCGTGGCTCCCATGCGCGGTGGACACAGATGACTGGTGTGTGCCACGCC 251
Db 275 ACTGTGGCGTGGGTGGCAGAGATCCCCCCAAGGATGCAACGGATCGCTGTCTGTCTCATC 334
Qy 252 ACAGACTGCTCTACGGGCGTCTGGAGAAGCTGGGGCTGTGAGCCCAAACTGGAAAAGTATC 311
Db 335 ATGACGTGTTCTACAAACGTTGGAGAAACGTGGATGTGCACCAAATTTCTGAGCTACA 394
Qy 312 TTTTCTCTGTACGGAACGTTGGCATTTTCTGGCGCGGCAGGACACCTGTCCACGGCGTGA 371
Db 395 AGTTTAGCACTCGGGAGGAGAATCACCTGTGCAAAACAGGACTCCTGCAGAAAGTCAAC 454
Qy 372 CCTGCGAGTGTGACAGAGGGCTGCCCTCTGCTTTTCCCGCAACTGGGGACCTTACAACC 431
Db 455 TGTGTAGTGTGATAGGCTGCTGCCACCTGTTTGTAGAAACAAGACGACCTACAATA 514
Qy 432 GCAAATATGCCATTATCCAAACAGTGTGCACCGGGCCCAACCCCGCCCTGCTGA 487
Db 515 AAAAGTACCAGTACTATTCCAAATAACACTGCAGAGGAGCACCCTCGTTGCTGA 570

RESULT 6
US-10-172-118-465
; Sequence 465, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Barnards, Rene
; TITLE OF INVENTION: diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 465
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens

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; CLONE: g190888
; SEQUENCE DESCRIPTION: SEQ ID NO: 1207 :
US-10-641-643-1207

Query Match      22.0%; Score 107.2; DB 16; Length 854;
Best Local Similarity 55.3%; Pred. No. 2.1e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGCTGGTGTCTCTTGGCTCTCTGGTGGCTCTGTCACCGGAACCTGGTTCAGTTTGGGG 134
DB 155 TGGCAGTGATCATGATCTTTGGCTTACTGCGAGGCCATGGGAATTTGGTGAATTTCCACA 214

QY 135 TGATGATCGAAGATGACAGGGAAG--TCCGCCCTGCGAGTACCAAGACTATGGGTGTT 191
DB 215 GAATGATCAAGTTGACGACAGGAAGAACGCGACTCAGTTATGGTCTTACGGCTGCC 274

QY 192 ACTCGGCATCGGTGGTCCCACTTGGCGGCGGAGACGACTGAGTGTGTGCGACGCC 251
DB 275 ACTGCGGTGGTGGCAGAGGATCCCAAGGATGCAACGGATCGCTGTGTCTCACTC 334

QY 252 ACGACTGCTGCTACGGGCTCTGAGAGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCT 311
DB 335 ATGACTGTGCTACAAACGCTGAGAAACGTTGATGTGGCACCACCAATTTCTGAGCTACA 394

QY 312 TTTTCTCTGTGTCAGGCAACGTGGCAATTTTCTGCGCGGCGAGCACCACTGCCAGCGGTGA 371
DB 395 AGTTTAGCACTCCGGGAGCAGATCACCCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 454

QY 372 CCTCGAGTGTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
DB 455 TGTGTGATGTGATAAGGCTGCTGCCACCTGTTTGTGCTAGAAACAGACGACCTACAATA 514

QY 432 GCAATATGCCATTATCCCAACAGCTGTGCAACGGGCGGCGGCGGCGGCGGCGGCTGCTGA 487
DB 515 AAAAGTACCAGTACTATTTCCAAATAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGA 570

RESULT 9
US-10-210-120-75
; Sequence 75, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-75

Query Match      22.0%; Score 107.2; DB 15; Length 967;
Best Local Similarity 55.3%; Pred. No. 2.2e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGCTGGTGTCTCTTGGCTCTCTGGTGGCTCTGTCACCGGAACCTGGTTCAGTTTGGGG 134
DB 292 TGGCAGTGATCATGATCTTTGGCTTACTGCGAGGCCATGGGAATTTGGTGAATTTCCACA 351

QY 135 TGATGATCGAAGATGACAGGCAAG---TCCGCCCTGCGAGTACCAAGACTATGGGTGTT 191
DB 352 GAATGATCAAGTTGACGACAGGAAGAACGCGACTCAGTTATGGTCTTACGGCTGCC 411
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QY 192 ACTGCGGCATCGGTGGCTCCCACTGGCGGCTGGACGACTGACTGGTGTGCTGCCAGGCC 251
DB 412 ACTGTGGCGTGGTGGCGAGAGATCCCCAAGAGATGCAACGATCGCTGCTGTGCTACTC 471

QY 252 ACGACTGCTGTACCGGCGTCTGGAGAGCTGGGCTGTGAGCCCCAACTGGAAAAAGTATC 311
DB 472 ATGACTGTTGCTACAAACGCTCTGGAGAAACGCTGGATGTGGCAACCAATTTCTGAGCTACA 531

QY 312 TTTTCTCTGTGACGAAAGTGGCATTTTCTGCGCGGCGGAGCACCACTGCCAGCGGTGA 371
DB 532 AGTTTAGCAACTCGGGGAGCAGAATCACCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 591

QY 372 CCTGCGAGTGTGACAGAGGCTGCCCTCTGCTTTTGGCGGCAACCTGGGCACTTACAACC 431
DB 592 TGTGTGAGTGTGATAAGGCTGCTGCCACCTGTTTGTGAGAAACAGACGACCTACAATA 651

QY 432 GCAATATGCCATTATCCCAACAGCTGTGCAACGGGCGGCGGCGGCGGCGGCTGCTGA 487
DB 652 AAAAGTACCAGTACTATTTCCAAATAAAGTGTGCTGCTGCTGCTGCTGCTGCTGA 707

RESULT 10
US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70

Query Match      22.0%; Score 107.2; DB 9; Length 1076;
Best Local Similarity 55.3%; Pred. No. 2.3e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGCTGGTGTCTCTTGGCTCTCTGGTGGCTCTGTCACCGGAACCTGGTTCAGTTTGGGG 134
DB 215 TGGCAGTGATCATGATCTTTGGCTTACTGCGAGGCCATGGGAATTTGGTGAATTTCCACA 274

QY 135 TGATGATCGAAGATGACAGGCAAG---TCCGCCCTGCGAGTACCAACGACTATGGGTGTT 191
DB 275 GAATGATCAAGTTGACGACAGGAAGAACGCGACTCAGTTATGGCTTCTACGGCTGCC 334

QY 192 ACTGCGGCATCGGTGGCTCCCACTGGCGGCTGGACGACGACTGACTGGTGTGCTGCCAGCCC 251
DB 335 ACTGTGGCGTGGTGGCGAGAGGATCCCAAGGATGCAACGGATCGCTGCTGTGCTCACTC 394

QY 252 ACGACTGCTGTACCGGCGTCTGGAGAGCTGGGCTGTGAGCCCCAACTGGAAAAAGTATC 311
DB 395 ATGACTGTTGCTACAAACGCTCTGGAGAAACGCTGGATGTGGCAACCAATTTCTGAGCTACA 454

QY 312 TTTTCTCTGTGACGAAAGTGGCATTTTCTGCGCGGCGGAGCACCACTGCCAGCGGTGA 371
DB 455 AGTTTAGCAACTCGGGGAGCAGATCACCCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 514

QY 372 CCTCGAGTGTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
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Db 515 TGTGTGAGTGTGATAAGGCTGTGCGCACCTGTTTGTGTAGAAACAAGACGACCTACAATA 574
QY 432 GCAATATGCCATTATCCCAACAAGCTGTGACCGGGCCACCCCGCCTGCTGA 487
Db 575 AANAAGTACCAGTACTATTCCATATAAACAAGTGCAGAGGAGGACCCCTGTGTTGCTGA 630

RESULT 11

US-09-740-569-1
; Sequence 1, Application US/09740569
; Publication No. US20020172668A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Jerrold
; APPLICANT: Elsbach, Peter
; APPLICANT: Liang, Ning-Sheng
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
; FILE REFERENCE: 5986/18917US1
; CURRENT APPLICATION NUMBER: US/09/740,569
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-740-569-1

Query Match 20.8%; Score 101.4; DB 9; Length 375;
Best Local Similarity 56.3%; Pred. No. 1.2e-21;
Matches 211; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 116 AACCTGGTTCAGTTTGGGTGATGATCGAGAGATGACAGGCAAG---TCCGCCCTGCAG 172
Db 1 AATTTGGTGAATTTCCACAGACTGATCAAGTTGACGACAGGAAAGGACCGCACTCAGT 60
QY 173 TACAAGCACTATGGCTGTGTACTCGGCATCGGTGGCTCCCACTGCGCGGTGACCACT 232
Db 61 TATGGCTTCTACGGCTGCCACTGTGGCGTGGTGAGAGATCCCAAGATGCAACG 120
QY 233 GACTGTGTGCTGCCACGCCACGACTGCTGTACGGCGCTCTGAGAGAGCTGGGCTGTGAG 292
Db 121 GATCGCTGTGTGCTCACTCATGCTGTGCTACAAACGCTGTGAGAAACGTTGGATGTGGC 180
QY 293 CCCAACTGGAAAGTATCTTTTCTGTCTGACGGAACGTGGCATTTTCTGCGCGCGGAGG 352
Db 181 ACCAAATTTCTGAGCTACAAGTTTAGCACTCGAAGACGAGAATCACCTGTGCAAAACAG 240
QY 353 ACCACCTGCAGCGGTGACCTCGAGTGTGACAGAGGGCTGCCCTCTGCTTTCGCCGC 412
Db 241 GACTCCTGCAGAGTCAACTGTGTGATGATAGGCTGTGCACTGTTTGTCTAGA 300
QY 413 AACCTGGGCACTACACCGGAAATATGCCCATTTATCCCAACAAGCTGTGACCGGGCCC 472
Db 301 AACAAAGAGACCTACAATAAAGTACCAGTACTATTCCATAAACAACACTGCAGAGGGAGC 360
QY 473 ACCCGCCCTGCTGA 487
Db 361 ACCCTCGTTGCTGA 375

RESULT 12

US-10-255-576-1
; Sequence 1, Application US/10255576
; Publication No. US20030161822A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Jerrold
; APPLICANT: Elsbach, Peter
; APPLICANT: Liang, Ning-Sheng
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
; FILE REFERENCE: 5986/18917US1

; CURRENT APPLICATION NUMBER: US/10/255,576
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/740,569
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-255-576-1

Query Match 20.8%; Score 101.4; DB 15; Length 375;
Best Local Similarity 56.3%; Pred. No. 1.2e-21;
Matches 211; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 116 AACCTGGTTCAGTTTGGGTGATGATCGAGAGATGACAGGCAAG---TCCGCCCTGCAG 172
Db 1 AATTTGGTGAATTTCCACAGACTGATCAAGTTGACGACAGGAAAGGACCGCACTCAGT 60
QY 173 TACAAGCACTATGGCTGTGTACTCGGCATCGGTGGCTCCCACTGCGCGGTGACCACT 232
Db 61 TATGGCTTCTACGGCTGCCACTGTGGCGTGGTGAGAGATCCCAAGATGCAACG 120
QY 233 GACTGTGTGCTGCCACGCCACGACTGCTGTACGGCGCTCTGAGAGAGCTGGGCTGTGAG 292
Db 121 GATCGCTGTGTGCTCACTCATGCTGTGCTACAAACGCTGTGAGAAACGTTGGATGTGGC 180
QY 293 CCCAACTGGAAAGTATCTTTTCTGTCTGACGGAACGTGGCATTTTCTGCGCGCGGAGG 352
Db 181 ACCAAATTTCTGAGCTACAAGTTTAGCACTCGAAGACGAGAATCACCTGTGCAAAACAG 240
QY 353 ACCACCTGCAGCGGTGACCTGCGAGTGTGACAGAGGGCTGCCCTCTGCTTTCGCCGC 412
Db 241 GACTCCTGCAGAGTCAACTGTGTGATGATAGGCTGTGCACTGTTTGTCTAGA 300
QY 413 AACCTGGGCACTACACCGGAAATATGCCCATTTATCCCAACAAGCTGTGACCGGGCCC 472
Db 301 AACAAAGAGACCTACAATAAAGTACCAGTACTATTCCATAAACAACACTGCAGAGGGAGC 360
QY 473 ACCCGCCCTGCTGA 487
Db 361 ACCCTCGTTGCTGA 375

RESULT 13

US-10-016-149-3
; Sequence 3, Application US/10016149
; Publication No. US20030100524A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP V (CA2+--
; TITLE OF INVENTION: DEPENDENT) EXPRESSION
; FILE REFERENCE: RTS-0325
; CURRENT APPLICATION NUMBER: US/10/016,149
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 3
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)...(549)
US-10-016-149-3

Query Match 20.5%; Score 99.8; DB 15; Length 1016;
Best Local Similarity 54.5%; Pred. No. 4.8e-21;
Matches 222; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

82	QY	GTTCCTTTGGCCTCCTGGTGGCTCTGCTACACGGGAACCTGGTTCAGTTTGGGGTGATGAT	141
159	Db	 GTTCTCTGGCTTGTAGTGTGCTGCTGTGCAAGAGAGGCTTGCTGGACTAAATCAATGAT	218
142	QY	CGAAGAGATCACAGGCGAAGTCCGCCCTG --- CAGTACAAAGCACTATGGCTGTGTACTGCGG	198
219	Db	 CGAAGAGGTACAGGGAAGAACCCTTGCAAACTTACGGCTTCTACGGCTTTTACTGCGG	278
199	QY	CATCGGTGGCTCCACTGGCCGGTGGACCAAGACTGACTGGTGTGCTGCCACGCCACGACTG	258
279	Db	 CTGGGCGCGCGAGGAACCCCAAGATGCCACCGATTGCTGTGTGGCGCGATGACCA	338
259	QY	CTGCTACGGCGCTGTGAGAAGCTGGGCTGTGAGCCCAAACTGGAAGATATCTTTTCTC	318
339	Db	CTGCTATATGGCGGCTGGAGGAGAAGGCTGCAACATTCGCACACAGTCTTACAAATACAG	398
319	QY	TGTCAGGGAAGTGGCACTTTTCTGGCCGGCAGAGACCCTGCCAGGGCTGACCTCGCA	378
399	Db	ATTTCGGGTGGGGGTGTGTACCTTCGAGCCCGGGCCCTTCTGCCCATGTGAACCTCTGTGC	458
379	QY	GTGTGACAAGAGGGCTGCCCTCTGCTTTCGCGCAACTCGGGCACCTTACAACCGCAATA	438
459	Db	CTGTGACCGGAAGCTGCTCTACTTGCTCTCAGAGNAACCTACGGAGCTACAACCCACAGTA	518
439	QY	TGCCCAATTATCCCAACAAGTGTGCACCGGGCCACCCCGCCCTGCT	495
519	Db	CCAATACCTTTCCCAACATCTCTGCTCTAGGCGCTCCCGACGAGCT	565

RESULT 14

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US-10-647-426-17
; Sequence 17, Application US/10647426
; Publication NO. US20040110197A1
; GENERAL INFORMATION:
; APPLICANT: Skinner, Michael K.
; APPLICANT: Patton, Jodi L.
; TITLE OF INVENTION: A METHOD OF DETERMINING TUMOR CHARACTERISTICS BY
; TITLE OF INVENTION: DETERMINING ABNORMAL COPY NUMBER OR EXPRESSION LEVEL OF
; TITLE OF INVENTION: LIPID-ASSOCIATED GENES
; FILE REFERENCES: PATRICK EAGLEMAN: EMBOL-X 252/124
; CURRENT APPLICATION NUMBER: US/10/647,426
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/03/676,052
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 17
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1016)
; OTHER INFORMATION: The sequence of the cDNA coding for Phospholipase
; OTHER INFORMATION: A2
; US-10-647-426-17

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	Query Match	20.5%	Score 99.8	DB 17	Length 1016
	Best Local Similarity	54.5%	Pred. No. 4.8e-21		
	Matches 222	Conservative 0	Mismatches 182	Indels 3	Gaps 1
Qy	82	GTTCCTTTGGCTCCTCGTGTGCTCTGTGTCACCGGGAACCTGTTTCAGTTTGGGGTGATGAT	141		
Db	159	GTTCCTCGCTTGTATGTGTGCTGTGTGCAAGGAGGCTTGTGACCTTAAATCAATGAT	218		
Qy	142	CGAAGATGACAGGCAAGTCGGCCCTG---CAGTACAAGCACTATGCGCTGTTTACTCGGG	198		
Db	219	CGAAGAGTGACAGGGAAGAAGCGCCCTTGACAACTACGGCTTCTACGGCTGTACTCGGG	278		
Qy	199	CATCGTGGTCCCACTCGGCGGTGGACCAAGACTGATGTGTGTGCCACGCCCAAGACTG	258		
Db	279	CTGGGCGGCGGAGGAACCCCAAGGATGGACCGATTTGTGCTGTGTGGCGGATGACCA	338		

[illegible]

RESULT 15

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US-10-198-846-10988
; Sequence 10989, Application US/10198846
; Publication NO. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10988
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1064, 1065, 1066, 1067, 1068
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-10988

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Query Match	20.4%;	Score 99.4;	DB 14;	Length 1068;
Best Local Similarity	55.6%;	Pred. No. 6.5e-21;		
Matches	232;	Conservative 0;	Mismatches 181;	Indels 4; Gaps 2
Qy	75	TGCTGGTTCCTTTGGCTCTCGTTCAGCGGACCTGGTTCAGTTTGGGG	134	
Db	244	TGCGAGTGATCATGATCTTTGGCCTACTGCAAGCCCATGGGAATTTGGTGAATTCACCA	303	
Qy	135	TGATGATCGAGAAGATGACAGGCAAG--TCGCGCCTTGCAGTACAAACGATATGGCTGTT	191	
Db	304	GAATGATCAAGTTGACGACAGAAAGGACCGCACTGATTATGGCTTCTACGGCTGCC	363	
Qy	192	ACTGCGGCATCGGTGGCTCCCACTGGCGGTGGACAGACTGACTGTGTGTGCCAGCCCC	251	
Db	364	ACTGTGGCTGGGTGGCAGAGATCCCCCAAGGATCAACGGATCGCTGTGTCTCACTC	423	
Qy	252	ACGACTGTGCTACGGGCGTCTGGGAGCTGGGCTGTGAGCCAAACTGGAAAGATC	311	
Db	424	ATGACTGTGTCTACAAACGCTCTGGAGAAACGTGATGTGGCACCAAATTTCTGAGCTACA	483	
Qy	312	TTTTCTCTGACGCAACGGTGCAATTTTCTCGCGCGGACAGCACCACTGGCAGCGGTGA	371	
Db	484	AGTTTAGCAACTCGGGGACGAGATCACTGTGCAAAACAGGATCTCTGCAGAGTCAAC	543	
Qy	372	CTTGGAGTGTGACAAGAGGGGTGCCCTCTCTGCTTTCGC-CGCAACCTGGGGACCTACAAC	430	
Db	544	TGTTGAGTGTGATTAAGGCTGCTGCACACTGTTTGTCTAGAAACAAGACGACCTACAAT	603	

Qy 431 CGAAATATGCCCATTTATCCCAACAAGCTGTGACGGGGCCACCCGGCCCTGCTGA 487
Db 504 AAAAGTACCAGTACTATTTCCAATAAACACTGCAGAGGGAGCACCCCTCGTTGCTGA 660

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Job time : 275 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 13, 2004, 05:00:27 ; Search time 1627 Seconds
(without alignments)
10907.283 Million cell updates/sec

Title: US-10-088-092A-29
Perfect score: 487
Sequence: 1 ctgctttcttctgctt.....ggccaccgccgctgtga 487

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463.4	95.2	465	AY417606	Homo sapi
2	308.8	63.4	464	AY417607	Pan trogl
3	308.6	63.4	462	AY417608	Mus muscu
4	308.6	63.4	537	BX519916	BX519916
5	308.6	63.4	728	BY741324	BY741324
6	307.8	63.2	726	CB597840	AGENCOURT
7	305.6	62.8	480	BE133458	UG33408.Y
8	260.6	53.5	381	BE128774	DEPA2524
9	217.4	44.6	436	BB851133	BB851133
10	190.4	39.1	320	AF046275	AF046275
11	188.2	38.6	309	CG473029	OST327 Mu
12	180.2	37.0	342	BY010605	BY010605
13	147.6	30.3	701	CF249871	esa005.e0
14	139.2	28.6	544	BB753895	BB753895
15	134	27.5	520	CD734010	CD734010
16	133.4	27.4	368	BY014871	BY014871
17	131	26.9	466	BE136551	UG33408.X
18	132	25.1	625	BO781867	UI-R-FFO-
19	115.2	23.7	549	BH358238	CH230-107
20	113.8	23.4	465	B3819195	B3819195
21	110.4	22.7	713	AZ661966	1M0540117
22	109.2	22.4	820	BQ483760	UI-H-EUO-
23	109	22.4	417	BQ031930	UI-1-CFO-
24	108.8	22.3	605	BM695558	UI-B-CQ1-

ALIGNMENTS

RESULT 1
AY417606
LOCUS Homo sapiens HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence, 465 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY417606
VERSION AY417606.1 GI:39773566
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 465)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 465)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source
1..465
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene
1..465
/locus_tag="HCM6280"

Query Match 95.2%; Score 463.4; DB 9; Length 465;
Best Local Similarity 99.8%; Pred. No. 7.5e-111;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 23 ATGCTCTTGTGACCTCCCTCCCGCAACCTGGGATGAATCTCCCGACGTCCTGGTG 82
Db 1 ATGCTCTTGTGACCTCCCTCCCGCAACCTGGGATGAATCTCCCGACGTCCTGGTG 60

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QY      83  TTCTTTTCCCTCCTGGTGGCTCTGGTCAACGGGAACCTGGTTCAGTTTGGGGTGATGTC 142
Db      61  TTCTTTTCCCTCCTGGTGGCTCTGGTCAACGGGAACCTGGTTCAGTTTGGGGTGATGTC 120

QY     143  GAGAAGATGACAGGCAAGTCCGCCCTGCGAGTACACGACTATGGCTGTACTGGCGCATC 202
Db     121  GAGAAGATGACAGGCAAGTCCGCCCTGCGAGTACACGACTATGGCTGTACTGGCGCATC 180

QY     203  GGTGGCTCCCACTGGCGGCTGGACAGACTGACTGGTGTGCGACGCCCAACACTGCTGC 262
Db     181  GGTGGCTCCCACTGGCGGCTGGACAGACTGACTGGTGTGCGACGCCCAACACTGCTGC 240

QY     263  TAGCGGGCTGTGAGAAGCTGGCTGTGAGCCCAACTGGAAGATATCTTTCTCTGTC 322
Db     241  TAGCGGGCTGTGAGAAGCTGGCTGTGAGCCCAACTGGAAGATATCTTTCTCTGTC 300

QY     323  AGCGACGTGGCAATTTCTGCGCGCGCAGACCACTGCGCGGCTGACCTGCGAGTGT 382
Db     301  AGCGACGTGGCAATTTCTGCGCGCGCAGACCACTGCGCGGCTGACCTGCGAGTGT 360

QY     383  GACAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGGCACCTACAAACGCAAAATATGCC 442
Db     361  GACAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGGCACCTACAAACGCAAAATATGCC 420

QY     443  CATTATCCCAACAGCTGTGCACCGGCGCCACCGCCCTGCTGA 487
Db     421  CATTATCCCAACAGCTGTGCACCGGCGCCACCGCCCTGCTGA 465

RESULT 2
AY417607 464 bp DNA linear GSS 12-DEC-2003
LOCUS Pan troglodytes HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY417607
VERSION AY417607.1 GI:39773567
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 464)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 464)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..464
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>464
/locus_tag="HCM6280"

gene
Query Match 63.4%; Score 308.8; DB 9; Length 464;
Best Local Similarity 67.5%; Pred. No. 3e-70;
Matches 313; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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QY     24  TGCTCTTGTGCACCTCCCTTCCCGCAACCTGGGATGAAATCTCCCCACGTCGTGTGT 83
Db      1  TGCTCTTGTGCACCTCCCTTCCCGCAACCTGGGATGAAACCTCCCCACGTCGTGTGT 60

QY     84  TCCTTTGCCCTCTGGTGGCTCTGCTCACCGGGAACCTGGTTCAGTTTGGGGTGATGTC 143
Db     61  TCCTTTGCCCTCTGGTGGCTCTGCTCACCGGGAACCTGGTTCAGTTTGGGGTGATGTC 120

QY    144  AGAAGATGACAGGCAAGTCCGCCCTGCGAGTACACGACTATGGCTGTACTGGCGCATCG 203
Db    121  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180

QY    204  GTGGCTCCCACTGGCGGCTGGACCGAGCTGACTGGTGTGCTGCCACGCCACGACTGCTGT 263
Db    181  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240

QY    264  ACGGGCGCTCGGAGAGCTGGGCTGTGAGCCCAACTGGAAGATATCTTTCTCTGTCA 323
Db    241  ACGGGCGCTCGGAGAGCTGGGCTGTGAGCCCAACTGGAAGATATCTTTCTCTGTCA 300

QY    324  GCGAACGTGGCAATTTCTGCGCGCGCAGGACCACTGCCAGCGGCTGACCTGCGAGTGT 383
Db    301  GCGAACGTGGCAATTTCTGCGCGCGTGGAGACCATCTGCCAGCGGCTGACCTGCGAGTGT 360

QY    384  ACAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGGCACCTACAAACGCAAAATATGCC 443
Db    361  ACAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGGCACCTACAAACGCAAAATATGCC 420

QY    444  ATTATCCCAACAGCTGTGCACCGGCGCCACCGCCCTGCTGA 487
Db    421  ATTATCCCAACAGCTGTGCACCGGCGCCACCGCCCTGCTGA 464

RESULT 3
AY417608 462 bp DNA linear GSS 12-DEC-2003
LOCUS Mus musculus HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY417608
VERSION AY417608.1 GI:39773568
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 462)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 462)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..462
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>462
/locus_tag="HCM6280"

gene

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Query Match      63.4%; Score 308.6; DB 9; Length 462;
Best Local Similarity 80.3%; Pred. No. 3.4e-70;
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 37 CCTCCCTTCCCGCAACCTGGGATGAATCTCCCACTGCTGGTGTCTTCTTCCCTCCT 96
   |||
Db 12 CCCCCTGCTACCTCCCGGAGATGAACCTCCCATGCTGCTTGCCTTTCCTCCT 71

QY 97 GGTGCTCTGGTACCGGGAACCTGTTCACTTGGGATGATGATCGAAGATGACAGG 156
   |||
Db 72 GGTGCTCTGGTACCGGGAACCTGTTCACTTGGGATGATGATGAGAGATGACAGG 131

QY 157 CAAGTCCGCTCGAGTCAACAGTATGGCTTTACTGCGGCTGCGTGGCTCCCACTG 216
   |||
Db 132 AAAGCTGCTCGAGTCAACAGTATGGCTTTACTGCGGCTGCGTGGCTCCCACTG 191

QY 217 GCCGCTGACAGTCACTGCTGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGGA 276
   |||
Db 192 GCCAGTGACAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 251

QY 277 GAAGCTGGGCTGAGCCCACTGGAAGATGATCTTCTGCTGCTGCTGCTGCTGCT 336
   |||
Db 252 GAAGCTGGGCTGAGCCCACTGGAAGATGATCTTCTGCTGCTGCTGCTGCTGCT 311

QY 337 TTCTGCGCGGCGAGGACACCTGCCAGCGGCTGACCTGCGAGTGTGCAAGAGGGCTGC 396
   |||
Db 312 CTCTGCTGCTGCTGAGAGCGCTGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCT 371

QY 397 CTCTGCTGCTGCGGCGAGGACACCTGCAACCGGCTGCTGCTGCTGCTGCTGCT 456
   |||
Db 372 TCTCTGCTGCTGCGGCGAGGACACCTGCAACCGGCTGCTGCTGCTGCTGCTGCT 431

QY 457 GCTGTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 487
   |||
Db 432 GCTGTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 462

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RESULT 4
BX519916
LOCUS
DEFINITION
IMAGE:1533423, mRNA sequence.
ACCESSION
BX519916
VERSION
BX519916.1 GI:32315712
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 537)
Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D.
and Korn, B.
Mouse Unigeneset - RZPD2
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998J163883.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse Unigeneset - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/ClonesCards/cgi-
bin/showLib.pl.cgi?response?libNo=981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD.
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
T7, Primer sequence: TATACGACTCACTATAGG.
FEATURES
Location/Qualifiers
1..537

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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE998J163883" ; IMAGE:1533423"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares NMPu"
/notes="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; 1st strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match      63.4%; Score 308.6; DB 5; Length 537;
Best Local Similarity 80.3%; Pred. No. 3.5e-70;
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 37 CCTCCCTTCCCGCAACCTGGGATGAATCTCCCACTGCTGGTGTCTTCTTCCCTCCT 96
   |||
Db 33 CCCCCTGCTACCTCCCGGAGATGAACCTCCCATGCTGCTTGCCTTTCCTCCT 92

QY 97 GGTGCTCTGGTACCGGGAACCTGTTCACTTGGGATGATGATCGAAGATGACAGG 156
   |||
Db 93 GGTGCTCTGGTACCGGGAACCTGTTCACTTGGGATGATGATGAGAGATGACAGG 152

QY 157 CAAGTCCGCTCGAGTCAACAGTATGGCTTTACTGCGGCTGCGTGGCTCCCACTG 216
   |||
Db 153 AAAGCTGCTCGAGTCAACAGTATGGCTTTACTGCGGCTGCGTGGCTCCCACTG 212

QY 217 GCCGCTGACAGTCACTGCTGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGGA 276
   |||
Db 213 GCCAGTGACAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 272

QY 277 GAAGCTGGGCTGAGCCCACTGGAAGATGATCTTCTGCTGCTGCTGCTGCTGCTG 336
   |||
Db 273 GAAGCTGGGCTGAGCCCACTGGAAGATGATCTTCTGCTGCTGCTGCTGCTGCTG 332

QY 337 TTCTGCGCGGCGAGGACACCTGCCAGCGGCTGACCTGCGAGTGTGCAAGAGGGCTGC 396
   |||
Db 333 CTCTGCTGCTGCTGAGAGCGCTTGCACGGGCTGCTGCGAGTGTGCAAGAGAGCTGC 392

QY 397 CTCTGCTTTCGCGCAACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 456
   |||
Db 393 TCTTGTGCTTTCGCGCAACCTGGAACCTTACAAACCGCAAGTATGCCCACTACCCCA 452

QY 457 GCTGTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 487
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Db 453 GCTGTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 493

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RESULT 5
BX741324
LOCUS
DEFINITION
BX741324 RIKEN full-length enriched, B16 F10Y cells Mus musculus
cDNA clone G37004420 5', mRNA sequence.
ACCESSION
BX741324
VERSION
BX741324.1 GI:27166149
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 728)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Saito, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

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/db_xref="taxon:10090"
/clone="IMAGE:30297098"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH_MGC_178"
/note="Organ: lung and heart; Vector: pDNR-LIB; Site: 1:
SfiI (ggccattatgcc); Site 2: SfiI (ggccctcgcc); cDNA
made by oligo-dT priming and directionally cloned. 5' and
3' adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGGCGGCGGATG-3' and
5'-ATTCTAGAGCGGAGGCGGCGGATG-3' (30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 63.2%; Score 307.8; DB 6; Length 726;
Best Local Similarity 82.1%; Pred. No. 5.9e-70;
Matches 354; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 57 GGATCAATCTCCCACTGCTGGTGTTCCTTTCCTCCTGCTGCTGTCACCGGA 116
DB 5 GGATGAACCTCCCACTGCTGGTGTTCCTTTCCTCCTGCTGCTGTCACCGGA 64
QY 117 ACCTGGTTCAGTTGGGCTGATGTCGAGAAATGACAGCAAGTCCGCTGTCAGTACA 176
DB 65 ACCTGGTCCAGTTGGAGTGTGATGTTGAGAAATGACAGCAAGTCCGCTGTCAGTACA 124
QY 177 AGGACTATGGCTGTACTCGGCATCGGTGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCT 236
DB 125 ATGACTATGGCTGTACTCGGCATCGGTGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCT 184
QY 237 GGTGCTGCCACGCCACGACCTGCTCTACGGGCGCTGTCGAGAAAGTGGGCTGTGAGCCCA 296
DB 195 GGTGTTGTATGCCATGACTGCTGCTATGGCGGCTGAGAGAGTGGGCTGTGAGCCCA 244
QY 297 AACTGGAAAAGTATCTTTCTGTGACGAAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
DB 245 AGCTGGAAAAGTATCTTTCTATCACTCGAGAACATCTTCTGTGCTGCTGCTGCTGCTGCT 304
QY 357 CTTGCCAGCGGCTACCTCGGAGTGTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
DB 305 CTTGCCAGCGGCTACCTCGGAGTGTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
QY 417 TGGGCACCTTACACCGCAAAATATGCCATTTATCCAAAGCTGTGCAACCGGCGCCACC 476
DB 365 TGAACACTTACAAACCGCAAGTATGCCACTACCCCAACAGCTGTGTACTGGGCGCCACC 424
QY 477 CCCTCTGCTGA 487
DB 425 CACCTGTGCTGA 435

RESULT 7

BE133458
LOCUS
DEFINITION
u933c08.y1 Soares_NMPu Mus musculus cDNA clone IMAGE:153423 5'
similar to SW:PA21_ERIMA P24293 PHOSPHOLIPASE A2 ISOZYME PLA-1 ;
mRNA sequence.
ACCESSION
BE133458
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 480)
REFERENCE
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
CONTACT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:949523
Seq primer: -40RP from Gibco
High quality sequence stop: 457.
Location/Qualifiers

FEATURES
source

1. 480
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:153423"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares NMPu"
/note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; 1st strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 62.8%; Score 305.6; DB 2; Length 480;
Best Local Similarity 80.1%; Pred. No. 2.1e-69;
Matches 359; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 37 CTTCCCTTCCCGCAACCTGGGATGAATCTCCCACTGCTGGTGTCTTCTTTCCTCTCT 96
DB 33 CCCCCTGCTTACCTCCCGCAGGATGAACCTCCCATGGCTGGCTTGCCTTTCCTCTCT 92
QY 97 GGTGGCTGTGTCACCGGAAACCTGTTTTCAGTTTGGGGTGTATGTCGAGAAATGACAGG 156
DB 93 GGTGGCTGTGTCACCGGAAACCTGTTTTCAGTTTGGGGTGTATGTCGAGAAATGACAGG 152
QY 157 CAACTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 216
DB 153 AAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 212
QY 217 GCGGTGGGACGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 276
DB 213 GCGGTGGGACGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272
QY 277 GAGCTGGGCTGTGAGCCCAACTGAAAGATATCTTCTCTGTGAGCAACGCTGGCAT 336
DB 273 GAAAGCTGGGCTGTGAGCCCAACTGAAAGATATCTTCTCTGTGAGCAACGCTGGCAT 332
QY 337 TTTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 396
DB 333 CTTCTGCTGCTGTAGAACGCTTGGCAGCGGCTGCTGCGAGGAGGAGGAGGAGGAGGAGGAG 392
QY 397 CTTCTGCTGCTGTGCGGCAACCTGGGCACTTACAAACCGGAAATATGCCCATTTATCCCAACAA 456
DB 393 TCTTGTGCTTTCGCGCAACCTGAAACCTTACAAACCGGCAAGTATGCCCACTACCCCAACAA 452
QY 457 GCTGTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 484
DB 453 GCTGTGACTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480

RESULT 8

BE128774
LOCUS
DEFINITION
DEP2524 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',
mRNA sequence.
ACCESSION
BE128774
VERSION
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 381)
Sleeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P., McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D.
Expressed sequence tags of cDNA clones from rat dermal papilla cells

Unpublished (2000)

Contact: Sleeman MA

Biological

Genesis Research and Development Corporation Limited

P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand

Tel: 0064 9 373 5600

Fax: 0064 9 373 2189

Email: m.sleeman@genesis.co.nz

Seq primer: T3 forward

High quality sequence stop: 381.

Location/Qualifiers

1..381

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Dark-Agouti"

/db_xref="taxon:10116"

/tissue_type="vibrissae"

/cell_type="dermal papilla"

/clone_lib="Rat Lambda ZAP Express Library"

ORIGIN

Query Match 53.5%; Score 260.6; DB 2; Length 381;
Best Local Similarity 83.4%; Pred. No. 1.3e-57;
Matches 296; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 98 GTGGCTCTGGTACCGGACCTGGTTCAGTTGGGTGATGATGAGAGATGACGCG 157

DB 27 GCGCCCTGGCTGGGACCTGGTCCAGTTGGAGTAATGATGAGAGATGACGGA 86

QY 158 AAGTCGGCTGTGAGCCCAAACTGGAAGATATCTTTCTCTGTCAGGCACTGGTCCCACTGG 217

DB 87 AAGCCGCTGTGATCCAACTGGAAGTACCTCTCTATCACCGGACACCAATC 146

QY 218 CGGTGGACAGACTGACTGTGCTGCCAGCCAGACTGTGCTAGCGGCTGTGAG 277

DB 147 CGGTGGACAGAGATGCTGTGCTGCCAGCCAGACTGTGCTAGCGGCTGTGAG 206

QY 278 AAGTCGGCTGTGAGCCCAAACTGGAAGATATCTTTCTCTGTCAGGCACTGGTCCCACTGG 337

DB 207 AAGTCGGCTGTGATCCAACTGGAAGTACCTCTCTATCACCGGACACCAATC 266

QY 338 TTCTGCGCGGAGGACACCTGCCAGCGCTGACCTGCGAGTGTGACAAGGCGCTGCC 397

DB 267 TTCTGCTGTGAGACGACTTGGCAGCGGACAGCTGTGAGTGTGACAAGAGAGCTGCC 326

QY 398 CTCTGCTTTTCGCGGACCTGGGACCTACACCGCAATATGCCCATATCCCA 452

DB 327 CTCTGCTTTTCGCGGACCTGGGACCTATATACCGCAATATGCTCACTACCCCA 381

RESULT 9

BB851133

LOCUS

DEFINITION

Clone G270014B19 5', mRNA sequence.

BB851133

BB851133.1 GI:17092587

EST.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 436)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saio, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, I., Watanabe, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

e mouse tissues.

Location/Qualifiers

1..436

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

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/clone="G270014B19"

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Best Local Similarity 73.4%; Pred. No. 3e-46;
Matches 278; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 37 CCTCCCTTCCCGCACTGGGATGAATCTCCACGCTGCTGGTTCCTTTCCTCTCT 96

DB 47 CCCCTGCTTACCTCCCGGAGTGAATCTCCATTCCTGCTGCTTTCCTCTCT 106

QY 97 GGTGGCTCTGGTCACCGGAACTGGTTCAGTTTGGGTGATGATCAGAGATGACAG 156

DB 107 GGTGGCTCTGGTCACCGGAACTGGTTCAGTTTGGGTGATGATGAGAGATGACAG 166

QY 157 CAAGTCGGCTCTGACGACAGACTATGGCTGTGTTACTGGGATGCTGGTTCCTCAT 216

DB 167 AAAGCTGGCTCTGACGACAGACTATGGCTGTGTTACTGGGATGCTGGTTCCTCAT 226

QY 217 GCGGTGGACGACGACTGCTGGTGTGCCACGACGCTGCTGACGGCGCTGGA 276

DB 227 GCAGTGGACGACGAGATGCTGTGTTGCTATGCCATGACTGCTGTATGGCGCTGGA 286

QY 277 GAAGCTGGCTGTGAGCCCAAACTGGAAGATATCTTTTCTGTGACGAGACGTGGCAT 336

DB 287 GAAGCTGGCTGTGAGCCCAAACTGGAAGATATCTTTTCTGTGACGAGAGAAACAT 346

QY 337 TTCTCTGGCGGACGAGACCACTGCCAGGCTGACCTGCGAGTGTGACAGAGGCTGC 396

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Db 347 CTTCTGTGCTGTAGAAAGCGTTGCCACCGGATACCTGCCAGCTGTGACAAAGAGCCG 406
Qy 397 CCTCTGCTTTGGCCGCAAC 415
Db 407 ATCTGCTTTGCCAAACC 425

RESULT 10
AF046275 320 bp DNA linear GSS 02-NOV-2000
LOCUS AF046275 Mus musculus 129Sv/Ev Mus musculus genomic clone OST327,
DEFINITION genomic survey sequence.
ACCESSION AF046275
VERSION AF046275.1 GI:3005146
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 320)
Zambrowicz,B.P., Friedrich,G.A., Buxton,B.C., Lillieberg,S.L.,
Person,C. and Sands,A.T.
Disruption and sequence identification of 2,000 genes in mouse
embryonic stem cells
NATURE 392 (6676), 608-611 (1998)
JOURNAL Nature 392 (6676), 608-611 (1998)
MEDLINE 98219085
PUBMED 9560157
COMMENT Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Omnibank Sequence Tag
Class: exon-trapped.
Location/Qualifiers
1..320
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Best Local Similarity 78.5%; Pred. No. 3.6e-39;
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

Qy 146 AAGATGACAGGCAAGTCCGCCCTGCAGTACACGACTATGGTGTGTTACTGCGGCATCGGT 205
Db 5 AAGAGANGAGGGAACCTGCCCTGNAGTACAACTNACTATGGTGTGTTACTGCGGTTCGGT 64
Qy 206 GGCTCCCACTGGCCGT-GGACCACTGACTGCTGCCAGCCAGCCAGCTGCTGTA 264
Db 65 GGCTCCCACTGGCCAGTGGAGCAACGGAATGGTGTGTTGTCATGCCCATGCTGCTTA 124
Qy 265 CGGGCTCTGGAGAACTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTCTGTCTAG 324
Db 125 TGCGCCCTGGGAANCTGGGCTGTGACCCCAAGCTGGAAAAGTACTCTCTCTATCAC 184
Qy 325 CGAAGCTGGGATTTCTGGCCGCGAGACCACTGCCAGCGGCTGACCTGGAGTGTA 384
Db 185 TCGAGACCAACATCTTCTGTGTGTTAAACGGGTTCGCAGCGGCATACCTGCGAATGTA 244
Qy 385 CAAGAGGGCTGCCCTCTGCTTCGCGCAACTGGGCACCTACAACCGCAATATGCCCA 444
Db 245 CAA-AAAACCGCTCTCTGCTTTCGCCACACACCTGAACCTTACACCGCAANTATGCCCA 303
Qy 445 TTATCCCAACAAGCTGT 461
Db 304 CTACCCCAACAAGCTGT 320
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LOCUS OST327 Mus musculus 129Sv/Ev Mus musculus genomic clone OST327,
DEFINITION genomic survey sequence.
ACCESSION CG473029
VERSION CG473029.1 GI:37223742
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 309)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,F., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..309
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Best Local Similarity 79.3%; Pred. No. 1.3e-38;
Matches 245; Conservative 0; Mismatches 62; Indels 2; Gaps 2;

Qy 154 AGGCAAGTCGCCCTCGAGTACACGACTATGGCTGTACTGGGCACTCGTGCTCCCA 213
Db 2 AGGGAACCTGCCCTGNAGTACATNACTATGGCTGTATTCGGTGTGCTCGTCCCA 61
Qy 214 CTGCCCGGT-GGACCACTGACTGGTGTGCCACGCCACGACTGCTGTACGGCGTC 272
Db 62 CTGCCCACTGGAGCAACCGAATGGTGTGTCTATGCCCATGACTGCTGTATGCCGCC 121
Qy 273 TGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTCTCTGTGAGCAAGTG 332
Db 122 TGGAGAACTGGGCTGTGAGCCCAAGCTGGAAAAGTACCTCTCTCTATCTACTGAGACA 181
Qy 333 GCATTTTCTGGCCGCGGAGGACCACTGCCAGCGGCTGACCTGCGAGTGTGACAAGAGG 392
Db 182 ACATCTTCTGCTGTGTTAAACCGCTTGGCAGCGGCATACCTGCGAATGTGACAA-AAAA 240
Qy 393 CTGCCCTCTGTTTTCGGCGCAACCTGGGCACCTACACCCGCAATATGCCCATATCCCA 452
Db 241 CCGCTCTCTGTTTTCGCCCAACCACTGAACACTTACAACCGCAANTATGCCCATACCCCA 300
Qy 453 ACAAGCTGT 461
Db 301 ACAAGCTGT 309
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RESULT 12
 BY010605
 LOCUS
 DEFINITION BY010605 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus
 musculus CDNA clone G730021C18 5', mRNA sequence.
 BY010605
 VERSION
 ACCESSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 342)
 Okazaki, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schinobach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
 Chotia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, I.A.,
 Fietcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayashizaki, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, J.,
 Sakakume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, W., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES
 source
 Location/Qualifiers
 1..342
 /organism="Mus musculus"
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 cDNA"

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 Best Local Similarity 79.7%; Pred. No. 1.7e-36;
 Matches 212; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
 QY 37 CCTCCCTTCCCGCAACCTGGATGAAATCTCCACGTCGTGCTGCTTTCCTTTCCTCTCT 96
 DB 77 CCCCTGCTACCTCCCGCAGGATGAAACCTCCCAATTCGCTTGCCTTTCCTCTCTCT 136
 QY 97 GGTGCTCTGTCTACCCGCGAACCTGTTTCAGTTTGGGGTGTATGATCGAGAAGATGACAGG 156
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 QY 157 CAAGTCCGCTCTGAGTACAACTATGCTGCTTACTGCGGATCGGTGCTGCTCCCACTG 216
 DB 197 AAGCTTCCCTGCTGAGTACAACTATGCTGCTTACTGCGGATCGGTGCTGCTCCCACTG 256
 QY 217 GCGGCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 276
 DB 257 GCGGCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 316
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 DB 317 GAAGCTGGGTGTGAGCCCAAACTGG 342

RESULT 13
 CF249871
 LOCUS
 DEFINITION esa005.e06 Eimeria tenella-infected caecal tonsil Gallus gallus
 cDNA, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 701)
 Wittzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J.,
 Chausse, A.M. and Zoorob, R.
 A collection of chicken ESTs from activated immune cells
 Unpublished (2003)
 Contact: Zoorob R
 UPR 1983
 CNRS
 7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France
 Tel: 33 1 49 58 35 00
 Fax: 33 1 49 58 33 81
 Email: zoorob@vif.cnrs.fr.
 Location/Qualifiers
 1..701
 /organism="Gallus gallus"
 /mol_type="mRNA"
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FEATURES
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 Location/Qualifiers
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 /organism="Gallus gallus"
 /mol_type="mRNA"
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 /clone_lib="Eimeria tenella-infected caecal tonsil"
 /note="Organ: Caecal tonsil; Vector: pTriplex2"

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3	476.4	97.8	478	9	BC069116 Homo sapi
4	427.4	87.8	429	6	CQ727197 Sequence
5	308.6	63.4	762	10	BC037524 Mus muscu
6	308.6	63.4	870	10	AF166098 Mus muscu
7	308.6	63.4	883	6	E37230
8	308.6	63.4	883	6	BD013141 A gene en
9	308.6	63.4	883	10	AF112984 Mus muscu
10	190.4	39.1	320	6	E37217
11	190.4	39.1	320	6	AF123128 A gene en
12	144	29.6	101824	9	AL358253 Human DNA
13	144	29.6	157470	2	AL360079 Homo sapi
14	115.2	23.7	239739	2	AC116054 Rattus no
15	115.2	23.7	282515	2	AC118094 Rattus no
16	110.4	22.7	155816	2	AC121105 Mus muscu
17	110.4	22.7	186608	10	AL844178 Mouse DNA
18	108.8	22.3	483	9	AY655695 Homo sapi
19	108.8	22.3	483	9	AY655696 Homo sapi

Db	421	CCCTGCTGA	429		
RESULT 5	BC027524				
LOCUS	MGC:41157 IMAGE:1533423				
DEFINITION	Mus musculus phospholipase A2, group IIE, mRNA (CDNA clone				
ACCESSION	BC027524				
VERSION	BC027524.1	GI:20380622			
KEYWORDS	MGC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1. (bases 1 to 762)				
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kertman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouford, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 762)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgabs@mail.nih.gov Tissue Procurement: Marcelo Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Luisa Prabhu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jacques Schein, Asim Siddiqui, Rob Holt, Marco Marra.				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 67 Row: K Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755091. Location/Qualifiers 1. .762 /organism="Mus musculus" /mol_type="mRNA"				
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lab_host="DH10B"					
notes="Vector: pT73-Pac"					
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ORIGIN					
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Best Local Similarity	80.3%;	Pred. No. 3.6e-67;			
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Db	213	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272			
QY	277	GAAGCTGGGCTGTGAGCCCAAACTGGAAAGTATCTTTCTCTGTCAGCGAAGTGGCAT 336			
Db	273	GAAGCTGGGCTGTGAGCCCAAACTGGAAAGTATCTTTCTCTGTCAGCGAAGTGGCAT 332			
QY	337	TTTCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 396			
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QY	397	CCTCTGCTTTCGCGCGCAACCTGGGCACTTACAAACCAATATGCCCATTTATCCCAACA 456			
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QY	457	GCTGTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 487			
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LOCUS	AF166098				
DEFINITION	Mus musculus group IIE secreted phospholipase A2 (Pla2g2e) mRNA, complete cds.				
ACCESSION	AF166098				
VERSION	AF166098.1	GI:6164697			
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
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REFERENCE	1 (bases 1 to 870)				
	AF166098				
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	complete cds.				
	AF166098				
	AF166098.1	GI:6164697			
	Mus musculus (house mouse)				
	Mus musculus				
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 870)				

AUTHORS Valentini, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.
TITLE On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II enzymes

J. Biol. Chem. 274 (44), 31195-31202 (1999)
JOURNAL 20002639
MEDLINE 10531313
PUBMED
REFERENCE 2 (bases 1 to 870)
AUTHORS Valentini, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France

FEATURES
source
1..870
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/chromosome="4"
1..870
/gene="Pla2g2e"
162..590
/gene="Pla2g2e"
/EC_number="3.1.1.4"
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/translation="MKPPIALACLLVPLAGNLVQGVNIERTMTGKPALQVNDYGC YCGVGGSHWPVDETDWCHADCCYGRLEKLCDPKLEKYLFSITRDNIFCAGRTAQ RHTCECDKRALCFRHLNLTNYRYHYHNPKNLCITGPTPPC"

ORIGIN

Query Match 63.4%; Score 308.6; DB 10; Length 870;
Best Local Similarity 80.3%; Pred. No. 3.6e-67;
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 37 CCTCCCTCCCGCAACCTGGAGTGAATCTCCCAAGTGTGGTGTCTCTTGGCTCCT 96
Db 140 CCCCCTGCTACTCCCGGAGAACCTCCCAATTCCTGCTTGGCTTGGCTTGGCTCCT 199
QY 97 GGTGGCTGTGGTACCGGGAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 156
Db 200 GGTGCCCTGGCTGGCGGGAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 259
QY 157 CAAGTCCGCTGAGTACACAGCTATGGCTGTATCTGGGGATCGGTGCTCCCACTG 216
Db 260 AAAGCCTGCCCTGAGTACACAGCTATGGCTGTATCTGGGGTGTATCGAGAGATGACAGG 319
QY 217 GCGGTGGACCACTGACTGGTGTGCGGCAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 276
Db 320 GCGGTGGACCACTGACTGGTGTGCGGCAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 379
QY 277 GAAGCTGGGCTGTGAGCGCCCAACTGGAAAGTATCTTTTCTCTCTGACGGAACGTGGCAT 336
Db 380 GAAGCTGGGCTGTGAGCGCCCAACTGGAAAGTATCTTTTCTCTCTGACGGAACGTGGCAT 439
QY 337 TTTCTGCGCGGCAAGGCACTCCAGCGGCTGACCTGGAGTGTGACAGAGGGGTGC 396
Db 440 CTTCTGTGCTGTAGAACGGTGTGCGAGCGGCACTCTGCGAGTGTGACAGAGGGGTGC 499
QY 397 CCTCTGCTTTCCGCGCAACCTGGGCACTTACAAACCGCAAAATATGCCCATTTATCCCAACA 456
Db 500 TCTCTGCTTTCCGCGCAACCTGGGCACTTACAAACCGCAAAATATGCCCATTTATCCCAACA 559
QY 457 GCTGTGACCGGGGCGCCCGCCCTGCTGA 487
Db 560 GCTGTGACTGGGGCGCCCGCCCTGCTGA 590

RESULT 7
E37230
LOCUS 883 bp DNA linear PAT 31-JAN-2002

DEFINITION Gene encoding novel mouse secretory phospholipase A2.

ACCESSION E37230
VERSION E37230.1 GI:18626640
KEYWORDS JP 2000166568-A/14.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 883)
AUTHORS Teshizaki, J., Suzuki, N. and Hanasaki, K.
TITLE Gene encoding novel mouse secretory phospholipase A2
JOURNAL Patent: JP 2000166568-A 14 20-JUN-2000;
SHIONOGI & CO LTD

COMMENT
OS Mus musculus (mouse)
PN JP 2000166568-A/14
PD 20-JUN-2000
PP 09-DEC-1998 JP 1998349604

PR JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI
PC C12N15/09, C07K16/40, C12N5/10, C12N9/16, C12Q1/44// (C12N15/09, PC C12R1:91),
PC (C12N5/10, C12R1:91), (C12N9/16, C12R1:91), C12N15/00, C12N5/00, PC (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)

CC
FH Key Location/Qualifiers
FT CDS (166)..(591)
FT mat_peptide (223)..(591).
FEATURES
source
1..883
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

ORIGIN

Query Match 63.4%; Score 308.6; DB 6; Length 883;
Best Local Similarity 80.3%; Pred. No. 3.6e-67;
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 37 CTTCCCTTCCCGCAACCTGGAGTGAATCTCCCAAGTGTGGTGTCTCTTGGCTCCT 96
Db 144 CCCCCTGCTACTCCCGGAGAACCTCCCAATTCCTGCTTGGCTTGGCTTGGCTCCT 203
QY 97 GGTGGCTGTGGTACCGGGAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 156
Db 204 GGTGCCCTGGCTGGCGGGAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 263
QY 157 CAAGTCCGCTGAGTACACAGCTATGGCTGTATCTGGGGATCGGTGCTCCCACTG 216
Db 264 AAAGCCTGCCCTGAGTACACAGCTATGGCTGTATCTGGGGTGTATCGAGAGATGACAGG 323
QY 217 GCGGTGGACCACTGACTGGTGTGCGGCAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 276
Db 324 GCGGTGGACCACTGACTGGTGTGCGGCAACCTGGTTCAGTTTGGGGTGTATCGAGAGATGACAGG 383
QY 277 GAAGCTGGGCTGTGAGCGCCCAACTGGAAAGTATCTTTTCTCTCTGACGGAACGTGGCAT 336
Db 384 GAAGCTGGGCTGTGAGCGCCCAACTGGAAAGTATCTTTTCTCTCTGACGGAACGTGGCAT 443
QY 337 TTTCTGCGCGGCAAGGCACTCCAGCGGCTGACCTGGAGTGTGACAGAGGGGTGC 396
Db 444 CTTCTGTGCTGTAGAACGGTGTGCGAGCGGCACTCTGCGAGTGTGACAGAGGGGTGC 503
QY 397 CCTCTGCTTTCCGCGCAACCTGGGCACTTACAAACCGCAAAATATGCCCATTTATCCCAACA 456
Db 504 TCTCTGCTTTCCGCGCAACCTGGGCACTTACAAACCGCAAAATATGCCCATTTATCCCAACA 563
QY 457 GCTGTGACCGGGGCGCCCGCCCTGCTGA 487
Db 564 GCTGTGACTGGGGCGCCCGCCCTGCTGA 594

RESULT 8
E37230
LOCUS 883 bp DNA linear PAT 31-JAN-2002

LOCUS BD013141 883 bp DNA linear PAT 02-AUG-2002
DEFINITION A gene encoding novel human secretory type phospholipase A2.
ACCESSION BD013141
VERSION BD013141.1 GI:22093330
KEYWORDS WO 0121775-A/14.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 883)
AUTHORS Ishizaki, J., Suzuki, N., and Hanasaki, K.
TITLE A gene encoding novel human secretory type phospholipase A2
JOURNAL Patent: WO 0121775-A 14 29-MAR-2001;
SHIONOGI & CO LTD, JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI
COMMENT OS Mus musculus (mouse)
PN WO 0121775-A/14
PD 29-MAR-2001
PF 18-SEP-2000 WO 2000JP006344
PR 21-SEP-1999 JP 99P 266616
PI JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI
PC C12N9/20, C12N15/55, C12P21/02, C12P21/06, C07K16/40 CC
PH Key Location/Qualifiers
FT CDS (166)..(591)
FT mat_peptide (223)..(591).
FEATURES
source
1..883
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
ORIGIN
Query Match 63.4%; Score 308.6; DB 6; Length 883;
Best Local Similarity 80.3%; Pred. No. 3.6e-67;
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 37 CTTCCCTTCCCGCAACCTGGGATGAATCTCCACAGTGTGGTTCCTTGGCTCCT 96
DB 144 CCCCCTGGCTACTCCCGCAGATGAACCTCCATTGCCCTGGCTTGGCTTCTCT 203
QY 97 GGTGGCTCTGGTCAACGGGAACCTGGTTCAGTTTGGGGTGTATGATCGAAGATGACAGG 156
DB 204 GGTGCCCTGGTGGTGGGGAACCTGGTCCAGTTTGGAGTGTATGATGAGAATGACCGG 263
QY 157 CAACTCCGCTGCAGTACAAAGTATCTTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 216
DB 264 AAGCTCGCTGCAGTACAAAGTATCTTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
QY 337 TTTCTCGCGCGGAGACCACTGCGAGGCTGACCTGCGAGTGTGACAGAGGCTGC 396
DB 444 CTTCTGTGTGTAGAAACCGCTTGCAGCGGATACCTGCGAGTGTGACAGAGAGCTGC 503
QY 397 CTTCTGCTTTCGCGCAACTGCGGCACTTACACCGCAATATGCCATTTATCCCAACA 456
DB 504 TCTTTGCTTTCGCGCAACTGCAACTTACACCGCAATATGCCATTTATCCCAACA 563
QY 457 GCTGTGACCGGCGCCACCGCCCTGCTGA 487
DB 564 GCTGTGTACTGGGCGCCACCGCCCTGCTGA 594
RESULT 9
AF112984 883 bp mRNA linear ROD 23-FEB-2000
LOCUS AF112984
DEFINITION Mus musculus secretory phospholipase A2 (Pla2) mRNA, complete cds.
ACCESSION AF112984

AF112984.1 GI:6651396
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 883)
AUTHORS Suzuki, N., Ishizaki, J., Yokota, Y., Higashino, K., Ono, T., Ikeda, M.,
Fujii, N., Kawamoto, K. and Hanasaki, K.
TITLE Structures, enzymatic properties, and expression of novel human and
mouse secretory phospholipase A(2)s
J. Biol. Chem. 275 (8), 5785-5793 (2000)
MEDLINE 20145788
PUBMED 10681567
REFERENCE 2 (bases 1 to 883)
AUTHORS Ishizaki, J., Suzuki, N., Higashino, K. and Hanasaki, K.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-1998) Shionogi Research Laboratories,
Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
FEATURES
source
1..883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
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/genes="Pla2"
166..594
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/note="sPLA2"
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ORIGIN
Query Match 63.4%; Score 308.6; DB 10; Length 883;
Best Local Similarity 80.3%; Pred. No. 3.6e-67; Indels 0; Gaps 0;
Matches 362; Conservative 0; Mismatches 89;
QY 37 CTTCCCTTCCCGCAACCTGGGATGAATCTCCACAGTGTGGTTCCTTGGCTCCT 96
DB 144 CCCCCTGGCTACTCCCGCAGATGAACCTCCATTGCCCTGGCTTGGCTTCTCT 203
QY 97 GGTGGCTCTGGTCAACGGGAACCTGGTTCAGTTTGGGGTGTATGATCGAAGATGACAGG 156
DB 204 GGTGCCCTGGTGGTGGGGAACCTGGTCCAGTTTGGAGTGTATGATGAGAATGACCGG 263
QY 157 CAACTCCGCTGCAGTACAAAGTATCTTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 216
DB 264 AAGCTCGCTGCAGTACAAAGTATCTTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
QY 337 TTTCTCGCGCGGAGACCACTGCGAGGCTGACCTGCGAGTGTGACAGAGGCTGC 276
DB 324 GCCAGTGGACGAGACGAGATTGGTGTCTCATGCCCATGACTGCTGTATGGCGCGCTGGA 383
QY 277 GAAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTCTGTCTGTCAGCAAGCTGGCAT 336
DB 384 GAAGCTGGGCTGTGAGCCCAAGCTGGAAAAGTATCTTTCTGTCTGTCATCTCGAGACAAT 443
QY 337 TTTCTCGCGCGGAGACCACTGCGAGGCTGACCTGCGAGTGTGACAGAGGCTGC 396
DB 444 CTTCTGTGTGTAGAAACCGCTTGCAGCGGATACCTGCGAGTGTGACAGAGAGCTGC 503
QY 397 CTTCTGCTTTCGCGCAACTGCGGCACTTACACCGCAATATGCCATTTATCCCAACA 456
DB 504 TCTTTGCTTTCGCGCAACTGCAACTTACACCGCAATATGCCATTTATCCCAACA 563
QY 457 GCTGTGACCGGCGCCACCGCCCTGCTGA 487
DB 564 GCTGTGTACTGGGCGCCACCGCCCTGCTGA 594

Db 564 GCTGTGTAAGTGGGCCACCCACCCCTGCTGA 594

RESULT 10
E37217
LOCUS
DEFINITION Gene encoding novel mouse secretory phospholipase A2.
ACCESSION E37217
VERSION E37217.1 GI:18626627
KEYWORDS JP 2000166568-A/1.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Ishizaki, J., Suzuki, N. and Hanasaki, K.
TITLE Gene encoding novel mouse secretory phospholipase A2
JOURNAL Patent: JP 2000166568-A 1 20-JUN-2000;
SHIONOGI & CO LTD

COMMENT
OS Mus musculus (mouse)
PN JP 2000166568-A/1
PD 20-JUN-2000
PF 09-DEC-1998 JP 1998349604

PR JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI
PC C12N15/09, C07K16/40, C12N5/10, C12N9/16, C12Q1/44// (C12N15/09, PC
C12R1:91),
PC (C12N5/10, C12R1:91), (C12N9/16, C12R1:91), (C12N15/00, C12N5/00, PC
(C12N15/00, C12R1:91), (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT source
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/db_xref="taxon:10090"

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Query Match 39.1%; Score 190.4; DB 6; Length 320;
Best Local Similarity 78.5%; Pred. No. 2.4e-37;
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

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146 AAGATGACAGGCAAGTCCGCTCGAGTACACAGCACTATGGTGTACTGGCGCATCGGT 205
5 AAGAGANGAGGGAACCTGCCCTGNAGTACAAATNACTATGGTGTATTGGGTGCGGT 64
206 GGCTCCCACTGGCCAGTGGGAGCAACGGAATGGTGTGTCATGCCCATGCTGCTA 264
65 GGCTCCCACTGGCCAGTGGGAGCAACGGAATGGTGTGTCATGCCCATGCTGCTA 124
265 CGGGCGCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTCTCTGTGAG 324
125 TGGCGGCTGGAGAACTGGGCTGTGACCCCAAGCTGGAAAAGTATCTTTCTCTATCAC 184
325 CGAAGCTGGCAATTTCTGCGCGGAGCAACCTGCCAGCGGTGACCTGCCAGTGTGA 384
185 TCGAGACAACATCTTCTGTGCTGTAACCGGCTGCCAGCGGCACTACCTGCGAATGTA 244
385 CAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGGCACTCAACCGCAAAATATGCCA 444
245 CAA-AAAACCGCTCTCTGCTTTGCGCGCAACCTGGAACACTTACACCGCAANTATGCCA 303
445 TTATCCCAACAGCTGT 461
304 CTACCCCAACAGCTGT 320

RESULT 11
BD013128
LOCUS
DEFINITION A gene encoding novel human secretory type phospholipase A2.
ACCESSION BD013128.1 GI:22093317
VERSION WO 0121775-A/1.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Ishizaki, J., Suzuki, N. and Hanasaki, K.
TITLE A gene encoding novel human secretory type phospholipase A2
JOURNAL Patent: WO 0121775-A 1 29-MAR-2001;
SHIONOGI & CO LTD, JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI

COMMENT
OS Mus musculus (mouse)
PN WO 0121775-A/1
PD 29-MAR-2001
PF 18-SEP-2000 WO 2000JP006344
PR 21-SEP-1999 JP 99P 266616
PI JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI
PC C12N5/20, C12N15/55, C12P21/02, C12P21/08, C07K16/40 CC
FH Key Location/Qualifiers
FT source
1. .320
/db_xref="taxon:10090"

ORIGIN
146 AAGATGACAGGCAAGTCCGCTCGAGTACACAGCACTATGGTGTACTGGCGCATCGGT 205
5 AAGAGANGAGGGAACCTGCCCTGNAGTACAAATNACTATGGTGTATTGGGTGCGGT 64
206 GGCTCCCACTGGCCAGTGGGAGCAACGGAATGGTGTGTCATGCCCATGCTGCTA 264
65 GGCTCCCACTGGCCAGTGGGAGCAACGGAATGGTGTGTCATGCCCATGCTGCTA 124
265 CGGGCGCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTCTCTGTGAG 324
125 TGGCGGCTGGAGAACTGGGCTGTGACCCCAAGCTGGAAAAGTATCTTTCTCTATCAC 184
325 CGAAGCTGGCAATTTCTGCGCGGAGCAACCTGCCAGCGGTGACCTGCCAGTGTGA 384
185 TCGAGACAACATCTTCTGTGCTGTAACCGGCTGCCAGCGGCACTACCTGCGAATGTA 244
385 CAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGGCACTCAACCGCAAAATATGCCA 444
245 CAA-AAAACCGCTCTCTGCTTTGCGCGCAACCTGGAACACTTACACCGCAANTATGCCA 303
445 TTATCCCAACAGCTGT 461
304 CTACCCCAACAGCTGT 320

RESULT 12
AL358253/c
LOCUS
DEFINITION Human DNA sequence from clone RP11-460G22 on chromosome 1, complete sequence.
ACCESSION AL358253
VERSION AL358253.16 GI:23304623
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Bagguley, C.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Sep 23, 2002 this sequence version replaced gi:22797900.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

AUTHORS
 TITLE
 JOURNAL
 COMMENT

McLay, K.
 Direct Submission
 Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 Requests: clonerequest@sanger.ac.uk
 On Aug 14, 2000 this sequence version replaced gi:8919533.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA6M4
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 1% of reads Chemistry:
 Dye-terminator Big Dye; 98% of reads
 Consensus quality: 145607 bases at least Q40
 Consensus quality: 150854 bases at least Q30
 Consensus quality: 153362 bases at least Q20
 Insert size: 15370; sum-of-contigs
 Insert size: 175968; 2.3% error; agarose-fp
 Quality coverage: 3.40x in Q20 bases; sum-of-contigs Quality
 coverage: 3.16x in Q20 bases; agarose-fp

During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw:
 SWISSPROT; Tr: TREMBL; Wp: WORMPEP; information on the WORMPEP
 database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
 Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
 RP11-460G22 is from the library RP11-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

FEATURES

Location/Qualifiers

1..101824
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 /clone="RP11-460G22"
 /clone_lib="RP11-11.2"

ORIGIN

Query Match 29.6%; Score 144; DB 9; Length 101824;
 Best Local Similarity 100.0%; Pred. No. 1.5e-25;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 344 GCCGCGAGACACCTGCGAGGCTGACCTGCGAGGTGACAGAGGCTGCCCTGTC 403
 Db 13902 GCCGCGAGACACCTGCGAGGCTGACCTGCGAGGTGACAGAGGCTGCCCTGTC 13843
 QY 404 TTTCGCCGCAACCTGGGCACTACACCGCAATATGCCATTATCCCAACAGCTGTGC 463
 Db 13842 TTTCGCCGCAACCTGGGCACTACACCGCAATATGCCATTATCCCAACAGCTGTGC 13783
 QY 464 ACCGGGCGCCACCCGCTGTGTA 487
 Db 13782 ACCGGGCGCCACCCGCTGTGTA 13759

RESULT 13

AL360079/c 157470 bp DNA linear HTG 10-JUL-2001
 LOCUS
 Homo sapiens chromosome 1 clone RP11-66M4, 22 unordered pieces.
 DEFINITION
 ACCESSION AL360079
 VERSION AL360079.3 GI:9801103
 KEYWORDS HTG; HTGS_PHAS51; HTGS_CANCELLED.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 22 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 15108: contig of 15108 bp in length
 15208: gap of 100 bp
 15209: contig of 4869 bp in length
 20177: gap of 100 bp
 20178: contig of 6421 bp in length
 26598: gap of 100 bp
 26599: gap of 100 bp
 31874: contig of 5176 bp in length
 31875: gap of 100 bp
 31975: gap of 100 bp
 39580: contig of 7606 bp in length
 39581: gap of 100 bp
 62977: contig of 23297 bp in length
 63078: gap of 100 bp
 75654: contig of 12577 bp in length
 75755: gap of 100 bp
 90667: contig of 14913 bp in length
 90668: gap of 100 bp
 93945: contig of 3178 bp in length
 94045: gap of 100 bp
 99022: contig of 4977 bp in length
 99023: gap of 100 bp
 101699: contig of 2577 bp in length
 101799: gap of 100 bp
 105241: contig of 3442 bp in length
 105242: gap of 100 bp
 105342: contig of 2197 bp in length
 107539: contig of 100 bp
 107639: gap of 100 bp
 111009: contig of 2647 bp in length
 111109: gap of 100 bp
 113755: contig of 100 bp
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 121297: contig of 7441 bp in length
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 125841: contig of 4445 bp in length
 125842: gap of 100 bp
 125942: contig of 3315 bp in length
 129257: gap of 100 bp
 129356: contig of 100 bp
 136269: contig of 6913 bp in length
 136270: gap of 100 bp
 136879: contig of 2510 bp in length
 136370

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Qy	464	ACGGGGCCCAACCGCCCTGCTGA	487
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RESULT 15			
AC118094/c			
LOCUS	AC118094	282515 bp	DNA linear HTG 15-NOV-2002
DEFINITION	Rattus norvegicus clone CH230-117D17, WORKING DRAFT SEQUENCE, 3 unordered pieces.		
ACCESSION	AC118094.6	GI:25009605	
VERSION	HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.		
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 282515)		
AUTHORS	Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Cesar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.S., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Guarnate, P., Haaland, W., Hamil, C., Hamilton, C., Hernandez, J., Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hodgson, A., Hoques, M., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hughes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jiang, H., Johnson, B., Johnson, K., Joive, A., Kapathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulisede, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, K., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaekwem, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., L., Puazo, N., Quiroz, J., Rachlin, B., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Speed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Taylor, C., Teimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlarczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Weinstock, G., and Gibbs, R.A.		
TITLE	Direct Submission		
JOURNAL	Unpublished		

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 239739)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24942319.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GSO
Center clone name: CH230-38C10
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 219221 bases at least Q40
Consensus quality: 222773 bases at least Q30
Consensus quality: 225047 bases at least Q20
Estimated insert size: 229739; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers

1. 239739
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-38C10"
160857..162689
name="wgs_contig"
note="wgs_contig"
/note="clone_boundary"
clone_end:T7
site:EcoRI
end_sequence: BH308572

FEATURES
source
misc_feature
misc_feature

ORIGIN
Query Match 23.7%; Score 115.2; DB 2; Length 239739;
Best Local Similarity 87.5%; Pred. No. 2.8e-18;
Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 344 CGCGCAGACCACTGCGGCTGACCTGCGGCTGAGTGTGACAGAGGGTGGCCCTGCG 403
Db 111562 CTGGTGAAGACACTTGGCAGCGGACAGCTGTGAGTGTGACAGAGAGTGGCCCTGCG 111621

Qy 404 TTTCGCCCAACCTGGGCACTTATAACCGCAATATGCCCACTTATCCCAACAGCTGTGC 463

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 282515)
Worley, K.C.

Direct Submission

Submitted (13-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 282515)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 15, 2002 this sequence version replaced gi:23265558.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GUXU

Center clone name: CH230-117D17

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 255167 bases at least Q40

Consensus quality: 258594 bases at least Q30

Consensus quality: 260981 bases at least Q20

Estimated insert size: 261710; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 221138: contig of 221138 bp in length

* 221139 221238: gap of unknown length

* 221239 280772: contig of 59534 bp in length

* 280773 280872: gap of unknown length

* 280873 282515: contig of 1643 bp in length.

FEATURES

source

1. .282515
/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-117D17"

330. .81776

/note="clone boundary

clone_end:17

site:

end_sequence:BH279848"

6087. .6517

/note="clone boundary

clone_end:Sp6

site:

end_sequence:BH279850"

misc_feature 221239. .222784
/note="wgs end extension
clone_end:Sp6"

ORIGIN

Query Match 23.7%; Score 115.2; DB 2; Length 282515;
Best Local Similarity 87.5%; Pred. No. 2.8e-18;

Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 344 GCCGCGAGGACCACTGCGCAGCGCTGACCTGCGGCTGACACAGAGGGCTGCCCTCTGC 403
DB 246335 GCTGGTAGAAGCACTTCCAGCGCAGACCTGTGAGTGTGACAGAGAGTGCCTCTGC 246276

QY 404 TTTCGCGCAACCTGGGCACTACACCGCAATATGCCAATATCCCAACAACTCTGC 463

DB 246275 TTTCGCCACAACTGGGCACTTATACCGCAAGTATCTACTACCCCAACAACTCTGC 246216

QY 464 ACCGGGCGCCACCCCGCCCTGCTGA 487

DB 246215 ACTGGGCGCCACCCCGCCCTGCTGA 246192

Search completed: November 13, 2004, 05:43:02
Job time : 1701 secs

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